SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:	The state of the s	Examiner #: Date:	
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Wall Box and Bldg/Room Loca	tion:	Results Format Preferred (circle): PAPER	DISK E-MAIL
If more than one search is su	bmitted, please ;	orioritize searches in order of need.	
Please provide a detailed statement of Include the elected species or structure utility of the invention. Define any telegram Please attach a copy of the cov	the search topic, and es, keywords, synonyr rms that may have a s ver sheet, pertinent cla	describe as specifically as possible the subject matter to us, acronyms, and registry numbers, and combine with pecial meaning. Give examples or relevant citations, a tims, and abstract.	be searched the concept or uthors, etc. ii
Inventors (also as a second of the		<u> </u>	
	i):		
Earliest Priority Filing Date:			
For Sequence Searches Only Please in appropriate serial number.	volude all pertinent info	rmation (parent, child, divisional, or issued patent numbers	i) along with the
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STAFF USE ONLY	Type of Search	Venders and east release 1	******
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Searcher Phone #: 272-25-26	AA Sequence (#)		
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rate Completed: 5/28/04			
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Online Lett. 27	Other	WWW/Internet	
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 26, 2004, 09:24:28; Search time 18 Seconds (without alignments) 1232.327 Million cell updates/sec Run on:

US-09-966-781A-1 2243 1 DQTALYIRWLGDVRVRSRAG......DTDAAFELNSQLLPQENRLS 426 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ol3946 homo sapien	m	P70453 mus musculu	Q9np56 homo sapien	Ξ	P54748 rattus norv	O89084 mus musculu	P14646 rattus norv	3 homo	Q08493 homo sapien) homo	homo) rattu	P14644 rattus norv	O60658 homo sapien	Snm	Q22000 caenorhabdi		P12252 drosophila			bos t	Q01065 mus musculu	Q01066 rattus norv	Q64338 mus musculu	Q63421 rattus norv	Q01064 homo sapien		P54750 homo sapien	рошо	30 bos	062	076083 homo sapien
SUMMARIES	ID	CN7A HUMAN	CN7A_RAT	CN7A MOUSE	CN7B HUMAN	CN7B_MOUSE	CN4A RAT	CN4A MOUSE	CN4B RAT	CN4B_HUMAN	CN4C_HUMAN	CN4D HUMAIN	CN4A HUMAN	CN4D_RAT	CN4C_RAT	CN8A HUMAN	CN8A MOUSE	YST1 CAEEL	YFGK_CAEEL	CNA1 DROME	REGA_DICDI	CNBB HUMAN	CNIB BOVIN	CNIB MOUSE	CNIB RAT	CN1C MOUSE	CN1C_RAT	CN1B HUMAN	CN1A MOUSE	CN1A HUMAN	CN1C HUMAN	CN1A BOVIN		CN9A_HUMAN
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o k	Query Match	00	94.3	٠				24.6						24.0	23.8			22.0	21.5	21.3	21.0	21.0	21.0	21.0	20.9	20.8	20.6	20.4	20.4	20.5	20.2	σ		18.4
	Score	224	2116	21.05	1403.5	1391.5	555	551	250	550	545	542	541	539	534.5	503	498.5	493.5	482	478.5	471.5	471.5	470.5	470.5	469.5	466	461	457.5	456.5	452	452	439.5	Н	412
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Q13370 homo sapien	Q63085 rattus norv	Q61409 mus musculu	Q14432 homo sapien	Q62865 rattus norv	077746 canis famil	076074 homo sapien	054735 rattus norv	Q8cg03 mus musculu	Q28156 bos taurus	P14099 bos taurus	Q01062 rattus norv
3B HUMAN	3B_RAT	A3B_MOUSE	NAMUH_HUMAN	CN3A_RAT	CN5A CANFA	CN5A HUMAN	NSA RAT	N5A MOUSE	CNSA_BOVIN	CN2A_BOVIN	CN2A_RAT
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ALIGNMENTS

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RESULT 2

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                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALKCADICNPCRTWELSKOWSEKVTBEFFHOGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 DOTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (POTENTIAL).
MEVCYCLPVLELDREPPQHYLSRRGAISFSSSSALFGCPNP
RQLSQ - MGITLINGLALVLIKWITSK (in isoform
PDE/A2).
                  DOMAIN: Composed of a C-terminal catalytic domain containing two putative divalent metal sites and an N-terminal regulatory domain. SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS
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MIM; JT1885; -.

GO; GO:0000267; C:cell fraction; NAS.

GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.

GO; GO:0007165; P:signal transduction; NAS.

InterPro; IPR003607; Met_phsphohydro.
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PROSTI; PROGGUZG; PEDBASE I; 1.

Hydrolase; CAMP; Phosphorylation; Alternative splicing.

DOMAIN 28 33 POLY-SER.

DOMAIN 47 451 CAPALYTIC (BY SIMILABITY).

MOD_RES 84 84 PHOSPHORYLATION (POTENTIAN ADD_RES) 1 46 MEVCYQLPVLPLDRRYPQHYLSRRG ROLSQ. > MGITLIWCLALVLIKW.
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3B3C8F6E9154F88C_CRC64;
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Pred. No. 1.4e-176;
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PRINTS; PR00387; PDIESTERASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- DOWAIN: Composed of a C-terminal catalytic domain containing two putative divalent metal sites and an N-terminal regulatory domain.
                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHAQSEIEASVSARNIRRLLSFQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoffmann R., Abdel'Al S., Engels P.; "Differential distribution of rat PDE-7 mRNA in embryonic and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..0
                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
41, Last annotation update)
High-affinity cAMP-specific 3', 5'-cyclic phosphodiesterase
(EC 3.1.4.17) (Rolipzam-insensitive phosphodiesterase type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 3.2e-166;
  426 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Cyclic nucleotide metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Biochem. Biophys. 28:103-113(1998)
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InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98176136; PubMed=9515162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 AA; 49274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00233; PDEase; 1.
PRINTS; PR00387; PDIESTERASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.3%;
94.1%;
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STANDARD;
                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; cAMP.
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                                                                                                                                                                                            Fragment).
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93.0.
Best Local Similarity 93.75
Matches 399; Conservative
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40,
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456 AA;
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Q9NP56;
16-OCT-2001
16-OCT-2001
15-MAR-2004
                                   family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
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CN7B HUMAN
ID CN7B HU
AC Q9NPE 6;
DT 16-OCT-
DT 15-MAR-
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LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
                                                                                                                  241 GLFSHLPLESRQOMETQIGALILATDISRQNEYLSEFRSHLDRGDLCLEDTRHRHLVLQM 300
                                                                                                                                           ALKCADICNPCRIWELSKOWSEKVTEBFFHOGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
                                                                                                                                                                                                                       MIYLVEPLFTEWARFSNIRLSQIMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
                                                                                                                                                                                                                                                                                                    VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKWTSVLENHHWRSAVGLLRES
                                                                VIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2).
SEQUENCE FROM N.A. (ISOFORM 2).
TISORIE-Brain, and Testis;
MEDLINE=20483661; PubMed=11027622;
Wang P., Wu P., Egan R.W., Billah M.M.;
"Cloning, characterization, and tissue distribution of mouse
phosphodiesterase 7AL.";
Blochem. Blophys. Res. Commun. 276:1271-1277(2000).
-!- FUNCTION: Plays a role in signal transduction by regulating the
intracellular concentration of cyclic nucleotides. This
phosphodiesterase is highly specific for cAMP and may have a role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     skeletal muscle.
DOMAIN: Composed of a C-terminal catalytic domain containing two
putative divalent metal sites and an N-terminal regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=2; Synonyms=PDE7A1;
IsoId=P70453-2; Sequence=VSP_004594;
IISSUE SPECIFICITY: Widely expressed with highest levels in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in muscle signal transduction. CATALYTIC ACTUTY Adenosine 3',5'-cyclic phosphate + H(2)O = adenosine 5'-cyclic phosphate + H(2)O = COFACTOR: Requires divalent cations.

ENZYME REGULATION: Insensitive to all selective PDE inhibitors. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN7A_MOUSE STANDARD; PRT; 456 AA.
P70453; Q9ERB3;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 43, Last annotation update)
High-affinity CAMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CAMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal muscle;
MEDLINE=97098542; PubMed=8943082;
Bloom T.J., Beavo J.A.;
"Identification and tissue-specific expression of PDB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphodiesterase splice variants.";
Proc. Natl. Acad. Sci. U.S.A. 93:14188-14192(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing, Named isoforms=2, Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=1; Synonyms=PDE7A2;
IsoId=P70453-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                              426
                                                                                                                                                                                                                                                                                                                                                                                                  QENRLS 426
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; kkuvu., ,
SMART; SM0471; HDC; 1.
PROSITE; PS00126; PDEAGE I; 1.
Hydrolase; cAmp; Alternative splicing.
DOMAIN 161 425 CAPALYTIC (BY SIMILARITY).
1 20 MGITLINCLALVLIKWITSK -> MEVCYQLPVLPLDRPVP
OHVLSRRGAISFSSSSALFGCPHPRQLSQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 YLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEXVGNWNFDIFLFDRLTNGNSLVSLTFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHIVIQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQTALYIRMLGDVRVRSRAGFESERRGSHPY1DFRIFHSQSE1EVSVSARNIRRLLSFQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSARNIRRLLSFQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLINGNSLVSLIFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 ALKCADICUPCRNWELSKQWSEKVTEBFFHQGDIEKKYHLGVSPLCDRQTBSIANIQIGF
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SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 456;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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93.7%; Pred. No. 2.8e-165;
ive 13; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP 004594.
A -> D (IN REF. 2).
0B826B96490D9F6E
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003607; Met_phsphohydro.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                         EMBL; U68171; AAB08479.1; -.
EMBL; AY007702; AAG16295.1; -.
                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00233, PDEase; 1.
PRINTS, PR00387, PDIESTERASE1.
SMART; SM00471; HDc; 1.
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52441 MW;
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240

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78 YFHASRLIRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH 137
                                           181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES
                              LFSLHGLIEYFHLDWWKLRRFLVWIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS
                                                                                                                                                                                                                                                                                                                                                    musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                             CN7B MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.
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                                                                                                                                                                             Sasaki T., Kotera J., Yuasa K., Omori K., "Identification of human PDE7B, a cAMP-specific phosphodiesterase."; Blochem. Blophys. Res. Commun. 271:575-583(2000).
                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 450;
                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1e-107;
66; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EC142BF3E28D0028 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.6%; Score 1403.5; DB 1;
                                                                                                                                                                   MEDLINE=20329226; PubMed=10872825;
                                                                                              MEDLINE=20275458; PubMed=10814504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB038040; BAA96537.1; -.
EMBL; AJ251860; CAB92441.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00387; PDIESTERASE1.
SMART; SM00471; HDc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00126; PDEASE I; 1.
Hydrolase; cAMP; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51835 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; JC7266, JC7266.
PDB; JLXW; 26-JUN-02.
Genew; HGNC:8792; PDE7B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00233; PDEase; 1
                     sapiens (Human)
                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           450 AA;
                                                                       SEQUENCE FROM N.A.
                                                     NCBI_TaxID=9606
                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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ACTAINTED. PLAN, No. 1

ACTAINTED. PLAN, No. 1

AGAGE TO STANDED. PLAN, Cawkill D., Fidock M.D.,
AGAGE TO STANDED. STAND
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                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                 377
                                     257
                                                                                    241 GLFSHLPLESROOMETOIGALILATDISRONEYLSLFRSHLDRGDLCLEDTRHRHLVLOM 300
                                                                                                                 ALKCADICNPCRIWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                             MIYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20087273; PubMed=10618442;
Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
"Cloning and characterization of PDE7B, a cAMP-specific phosphodiesterase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          090X01;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
15-MAR-2004 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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YLRSSRFFRGTAVSNSINILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR

18 61

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GLFSHLPLESRQQMETQIGALILATDISRQNBYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALKCADICNPCRIWELSKOWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 LENSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAADVTQAMHCYLKEPKLASF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR
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MEDLINE=89264472; PubMed=2542942;
Davis R.L., Takayasu H., Eberwine M., Myres J.;
"Cloning and characterization of mammalian homologs of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentía, Sciurognathi, Muridae, Murinae, Rattus.
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 MIYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGL----QREQSSSED 407
EMBL; AF190639; AAF25195.1; -.
EMBL; AJ51859; CAB9530.1; -.
MGD; MGI:135.75; Pde7b.
GO; GO:0004115; F:CAMP-specific phosphodiesterase activity; IDA.
InterPro; IPR003607; Met_phsphohydro.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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                                                                                                                                                                                                                                                                                                      CATALYTIC (BY SIMILARITY)
7C052664B693A5A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dunce+ gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:3604-3608(1989)
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SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4 AND 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIŜSUB=Brain;
MEDLINE=95047482; PubMed=7958996;
Bolger G.B., Rodgers L., Riggs M.;
                                                                                                                               InterPro; IPR002073; PDEase.
Pfam; PF00233; PDISSE; 1.
PRINTS; PR00387; PDIESTERASE1.
SWART; SW00411; HDC; 1.
PROSITE; PS00126; PDEASE_I; 1.
                                                                                                                                                                                                                                                                                                 172 410 CJ
446 AA; 51337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              256; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                     Hydrolase; CAMP.
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96779244; PubMed=8663181;
Smith K.J., Scotland G., Beattie J., Trayer I.P., Houslay M.D.;
"Determination of the structure of the N-terminal splice region of
the cyclic AMP-specific phosphodiesterase RD1 (RNPDE4A1) by 1H NMR
and identification of the membrane association domain using chimeric
                                                                                                                                                                                                                                                         TISSUE=Testis;
MEDLINE=89315790; PubMed=2246153;
Swinnen J.V., Joseph D.R., Conti M.;
"Molecular cloning of rat homologues of the Drosophila melanogaster dunce CAMP phosphodiesterase: evidence for a family of genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).

    J. Biol. Chem. 271:16703-16711 (1996).
    -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)0 = adenosine 5'-phosphate.
    -!- ENZIME REGULATION: Inhibited by rolipram.
    -!- PATIMAY: Cyclic molectide metabolism.
    -!- ALTERNATIVE PRODUCTS:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=5; Synonyms-Short;
IsoId=P54748-5; Sequence=VSP 004569, VSP 004570;
TISSUE SPECIFICITY: Isoform 2 is testis specific.
SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE-Sprague-Dawley; TISSUE=Testis;
MEDLINE-96122847, FubMed=8557632,
Bolger G.B., McPhee I., Houslay M.D.;
"Alternative splicing of cAMP-specific phosphodiesterase mRNA transcripts. Characterization of a novel tissue-specific isoform,
       the
"Differential CNS expression of alternative mRNA isoforms of mammalian genes encoding cAMP-specific phosphodlesterases."; Gene 149:237-244(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSP 004567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                       SEQUENCE OF 319-677 FROM N.A. (ISOFORM 3/4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P54748-3; Sequence=VSP_004566,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=2; Synonyms=PDE4A8;
IsoId=P54748-2; Sequence=VSP_004565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=4; Synonyms=Medium;
Isold=P54748-4; Sequence=VSP_004568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1;
IsoId=P54748-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMEL, L27062, AAAA6899.1;
EMEL, M2548; AAA41848.1;
EMEL, M28411, AAA41888.1;
EMEL, M26715; AAA41803.1;
EMEL, M26715; AAA41101.1;
EMEL, M26715; AAA41101.1;
EMEL, M26717, AAA41102.1;
P.R., I53865; I53865.
PR, I67946; I67946.
PDB, HLOL, HSRNOYS, MELPhohydro.
InterPro; IPR003607; MeLphsphohydro.
                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 1-26 OF ISOFORM 3.
                                                                                                                                                                                                     J. Biol. Chem. 271:1065-1071(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00233; PDEase, 1.
PRINTS, PR00387; PDIESTERASE1.
SMART; SM00471; HDc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L27057; AAC27098.1; -. EMBL; L36467; AAB00357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      constructs.";
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263 RELTHLSEMSKSGNQVSEYISNTFLD----KQNEVEIPSPTPRQR---AFQQPPPSVLR 314
                                                                                                                                                                                                                                                                                                                                                           SSR-----FFRGTAVSNSLNI-----LDDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG 111
                                                                                                                                                                                                                                                                                                                                                                             112 NSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171
                                                                                                                                                                                                                                                                                                                                                                                                                        LKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR 63
PROSITE; PS00126; PDEASE I; 1.

Hydrolase; cAMP; Alternative splicing; Multigene family; 3D-structure.

VARSPLIC 1 102

RIQORGYPDSAERSETERSPHRPIERADAVOTGDREGLRTT

RIQORGYPDSAERSETERSPHRPIERADAVOTGDREGLRTT
                                                                                    Missing (In isoform 3).
/FIId=VSP_004566.
WCLEQLETMQTYRSVSEMASHK -> MPLVDFFCETCSKPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAVGLLRESG--LFSHLPLESRQOMETQIGALILATDISRQNEYLSLFRSHLD-----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTERFFHQGDIEKKYHLGVS
                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                     24.7%; Score 555; DB 1; Length 844; 32.6%; Pred. No. 1.1e-37; ive 77; Mismatches 154; Indels
                                                                                                                     IVGWWDQ (in isoform 3).
/FIId=VSP 004567.
Missing (in isoform 4).
/FIId=VSP 004568.
Missing (in isoform 5).
                                                                                                                                                                                                                                               1A5F5101E4DBF1B6 CRC64;
                                                                                                                                                     /FIIG=VSP 004568
Missing (In isoform 5).
/FIId=VSP 004569.
Missing (In isoform 5).
/FIId=VSP 004570.
GV -> AL (IN REF. 4).
GD -> AH (IN REF. 4).
                                                                  (in isoform 2).
                                                                               004565
                                                                                                                                                                                                                                      (IN REF.
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                                                                           FTIG=VSP
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                                                                                                                                                                                                                                                93438 MW;
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Best Local Similarity 32.6
Matches 127; Conservative
                                                                                                                                                                                                            466
604
833
                                                                                      234
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                                                                                                                                                                    318
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                                                                                                                                                                                                            465
603
833
844 AA;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                            CONFLICT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
           CN4A MOUSE STANDARD; PRT; 844 AA.
C89084; Q8RO78; Q9UHQ4; Q9QX48; Q9QX18;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
CAMP-dependent 3',5'-cyclic phosphodiesterase 4A (BC 3.1.4.17).
                                                                                                                                                                                               (1)
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
TISSUB=Embryonic stem cells;
MEDLINE=20069070; Pubmed=10602991;
                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                               PDE4A.
CN4A_MOUSE
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EMBL; AF142646; AAF14519.1; -. EMBL; AF142643; AAF14519.1; JOINED. EMBL; AF142644; AAF14519.1; JOINED.

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RECOMPLEAS SALIVARY Gland,

RECOMMESCASING STORM AND AND AND ALESCHESALIVARY GLAND AND ALESCHESALIVARY GLAND AND ALESCHESALIVARY GLAND ALESCHES R. Grausber R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Anderina R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Anderhenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schaefer C.F., Bat S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J., Berowstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C., R. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., R. Richards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gunsarane P.H., R. Richards S., Worley K.M., Sodergren B.J., Lu X., Gibbs R.A., Allalon D.K., Muzny D.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rhey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rhey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Raheseley R.W., Touchman J.W., Green E.D., Dickson M.C., Allakesley R.W., Krzywinski M.I., Skalska U., Smailus D.E., Retreffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length D.M., Phone M. P. Mann and mouse colby sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sullivan M., Rena G., Begg F., Gordon L., Olsen A.S., Houslay M.D., "Identification and characterization of the human homologue of the short PDE4A cAMP-specific phosphodiesterase 4A variant RDI (PDE4AI) by analysis of the human HSPDE4A gene locus located at chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                  "Physical mapping and promoter structure of the murine cAMP-specific phosphodiesterase pde4a gene."; Mamm. Genome 11:41-45(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isoid=089084-3; Sequence=VSP 004562;
SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                           Cherry J.A., Thompson B.E., Pho V., "Diazepam and rolipram differentially inhibit cyclic AMP-specific phosphodiesterases PDE4A1 and PDE4B3 in the mouse."; Biochim. Biophys. Acta 1518:27-35 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19p13.2.",
Biochem J. 333:693-703 (1998).
-!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O
adenosine 5'-phosphate.
-!- ENZYME REGULATION: Inhibited by rollipram and diazepam.
-!- PATHWAY: Cyclic nucleotide metabolism.
                                                                                                                (ISOFORM 2), AND ENZYME REGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSP_004564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 248-355 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=089084-1; Sequence=Displayed;
                                                                                                                                                    MEDLINE=21167368; PubMed=11267656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=98343959; PubMed=9677330;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 3).
  A.E., Bolger G.B.;
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=3
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Steele M.R.,

A.H.,

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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                       "Isolation and characterization of a mammalian gene encoding a high-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=89315790; PubMed=2546153;
Swinnen J.V., Joseph D.R., Conti M.;
"Molecular Cloning of rat homologues of the Drosophila melanogaster
dunce camp phosphodiesterase: evidence for a family of genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
                                                                                                                                                                                                                                                                                                             icelli J., Birchmeier C., Michaeli T., O'Neill K., Riggs M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bolger G.B., Rodgers L., Riggs M., "Differential CNS expression of alternative mRNA isoforms of mammalian genes encoding cAMP-specific phosphodiesterases.";
                                                                                                                                                             Huston E., Simon L., Annette R., Catterall C., Ross A.H. Bolger G.B., Perry M., Owens R., Houslay M.D., Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                             affinity CAMP phosphodiesterase.";
Proc. Natl. Acad. Sci. U.S.A. 86:3599-3603(1989).
                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM PDE4B3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM PDE4B2)
MEDLINE=95047482; PubMed=7958996;
                                                                                                                                                                                                                                                                                             MEDLINE=89264471; PubMed=2542941;
                                                                                                                                                                                                                                                   SEQUENCE OF 160-721 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 289-638 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammalian genes encodin
Gene 149:237-244(1994).
                                                                                                   NCBI_TaxID=10116;
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               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 FDRLINGNSLVSLIFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 VSEYAGGRSLSCIMYTIFQERDLIKKFHIPVDTMMTYMLTLEDHYHADVAYHNSLHAADV 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 PMSQITGLKKLVH-----TGSLNINVPREGVKIDQEDLLAQELENLSKWGLNIFC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEK 336
                                                                                                                                                                                                   Interro; IPR002u,,,...
Interro; PEam; PDEABE; 1.
PEam; PP00233; PDEABES; 1.
SMART; SM0471; PDEABE; SM0471; HDc; 1.
SMART; SM0471; HDc; 1.
PROSITE; PS00126; PDEABE I; 1.
Hydrolase; CAMP; Alternative splicing; Multigene family.
MRPPARPERSESISLEPERSPREQGATIKPPPQHLWRQPRTPI
WARSPLIC I 102 MRSPARRESEPERSPREADANDTGDRPGIRTI
RMSWPSSFHGTGGGGSSRR -> MRSSAARARPRPBALA
RMSWPSSFHGTGGGGSSRR -> MRSSAARARPRPBALA
THESFEREDTLRHPPGRCVS (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VSAR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform 2).
/FITG=VSP 004563.
LVGWMDO (in isoform 2).
/FITG=VSP 004564.
/FITG=VSP_004564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 TQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENHHWRSAVGLLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548 TXKVISSGVLLDDNYSDRIQVLRNWVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.6%; Score 551; DB 1; Length 844; 31.0%; Pred. No. 2.2e-37; ive 79; Mismatches 149; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632396C9F70E0F61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 KYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFTEWA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R -> K (IN REF. 2)
S -> G (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTId=VSP 004562
                                                                                    EMBL, AJ297396; CAB96769.1; --
EMBL, BC027224, AAR7224.1; --
EMBL, AR208021, AAR7224.1; --
EMBL, U97586; AAC75681.1; --
EMBL, U97586; AAC75681.1; --
InterPro, IPR003607; Met_phsphohydro.
AF142645; AAF14519.1; JOINED.
AF142644; AAF14520.1; -,
AF142644; AAF14520.1; JOINED.
AF142645; AAF14520.1; JOINED.
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Best Local Similarity 31.00
The 123; Conservative
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685
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685
844 AA;
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CONFLICT
SEQUENCE
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                                          EMBL;
                                                                  MBL;
  DR CORRESPONDED CO
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                                                                                                                                                                                                                                      Monaco L., Vicini E., Conti M.;
"Structure of two rat genes coding for closely related rolipram—
"Structure of two rat genes coding for closely related rolipram—
from alternative cAMP phosphodiesterases. Multiple mRNA variants originate
from alternative splicing and multiple start sites.";
J. Bloi. Chem. 269:347-357(1994).
-!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)0 =
adenosine 5'-phosphate.
-!- PAZXME REGULATION: Inhibited by rolipram.
-!- PAZMANY: Cyclic nucleotide metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=P14646-2; Sequence=VSP 004573;
-!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing, Named isoforms=3;
   Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P14646-3; Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P14646-1; Sequence=Displayed;
FROM N.A. (ISOFORM PDE4B2).
                                                                                                                                                                        MEDLINE=94103234; PubMed=8276818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=PDE4B3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=PDE4Bl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=PDE4B2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J04563; PEMBL; M25350; PEMBL; M28413; PEMBL; M28413; PEMBL; M28413; PEMBL; M28413; PEMBL; PEMB
                                                                                        STRAIN=Wistar;
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L27058; AAA74478.1; U01291; AAA18926.1; AAA41824.1;

EMBL; EMBL;

114646. 01-APR-1990 (Rel. 14, Created) 15-JUJ-1998 (Rel. 36, Last sequence update) 28-FBE-2003 (Rel. 41, Last annotation update) CAMP-specific 3',5'-cyclic phosphodiesterase 4B (EC 3.1.4.17) (DPDE4).

721 AA

STANDARD;

CN4B RAT

RESULT 8

CN4B RAT ID CN4B AC P146 DT 01-A DT 15-J DT 28-F DE CAMP DE CAMP

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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L20966; AAA03589.1; -.
EMBL; L20971; AAA03593.1; -.
EMBL; M97515; AAA36426.1; -.
EMBL; U85048; AAB96381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:8781; PDE4B
MIM; 600127; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, 161354, 161354.
PDB, 1F0J, 26-JUL-00.
PDB, 1JP1, 16-JAN-02.
PDB, 1JP2; 16-JAN-02.
                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=PDE4B2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=PDE4B3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=PDE4B1
                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; cAMP; Alternative splicing; Multigene family.
VARSPLIC 1 196 MTAKNSSKELPASESEVCIKTFKEQMRLELELPKLPGNRPT
                                                                                                                                                                                                                                                         SPKISPRSSPRNSPCFFRKLLVNKSIRQRRRFTVAHTCFDV
BNGPSPGRSPLDPOASSSGLVLHAAFPGHSQRRESFLYRS
                                                                                                                                                                                                                                                                                                   RNNFTLLTNIHGAPNKRSPAÅSQAPVTRVSLQ --> MKEQG
GTVSGAGSSRGGGDSAMASLQPLQPNYLSVCLFA (in
                                                                                                                                                                                                                                                                                        DSDYDLSPKAMSRNSSLPSEQHGDDLIVTPFAQVLASLRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR------LLLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELITHLSEMSRSGNOVSEYISNIFLD-----KONDVEIPSPIOKDREKKKKQQLMTQISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 ANSVIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 TFHLESLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
cAMP-specific 3',5'-cyclic phosphodiesterase 4B (EC 3.1.4.17)
                                                                                                                                                                                                                                                                                                                                                                                                        Length 721;
                                                                                                                                                                                                                                                                                                                                                                                                                                  152; Indels
                                                                                                                                                                                                                                                                                                                                               FTId=VSP 004573.
-> S (IN REF. 5).
C6FB885E6107BD4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     24.5%; Score 550; DB 1; 31.8%; Pred. No. 2.2e-37;
                                                                                                                                                                                                                                                                                                                                isoform PDE4B2)
/FTId=VSP 00457
T -> S (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                    R EMBL; U01295; AAA18926.1; JOINED.
RMBL; U01296; AAA18926.1; JOINED.
RMBL; U01297; AAA18926.1; JOINED.
RMBL; U01299; AAA18926.1; JOINED.
RMBL; U01299; AAA18926.1; JOINED.
PIR; A40949; AAA18926.1; JOINED.
PIR; JS9143; TF0745.
                                                                                                                                         InterPro; IPR003607; Met_phsphohydro.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |: |:||: || TASVEKSQVGFIDYIVHPLWETWA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TESIANIQIGEMTYLVEPLETEWA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                84;
                                                                                                                                                                                                                                                                                                                                                          516 T. B2100 MW;
                                                                                                                                                                    PFam, PF00233; PDEase; 1.
PRINTS, PR003947; PDIESTERASE1.
SMART; SM0471; HDC; 1.
PROSITE; PS00126; PDEASE_I; 1.
AAA18926.1;
AAA18926.1;
AAA18926.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD:
                                                                                                                                                                                                                                                                                                                                                           516 5
721 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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ID CN4B HI

OCO1343,
DT 01-FEB,
DT 01-FEB,
DE CAMP-SI

DE CAMP-SI

OCS HOMO SE

COS HOMO SE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not remoyed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                        [2] SEQUENCE FROM N.A. (ISOFORM PDE4B3).
MEDLINE-98041898; PubMed-9317114;
Huston E., Lumb S., Russell A., Catterall C., Ross A.H., Steele M.R.,
Bolger G.B., Perry M.J., Owens R.J., Houslay M.D.;
"Molecular cloning and transient expression in COS7 cells of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q07343-3; Sequence=VSP 004571;
TISSUB SPECIFICITY: Expressed In brain, heart, lung and skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue distribution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B101. Chem. 268:64/0-64/0 (1993).
FUNCTION: May be involved in mediating central nervous system effects of therapeutic agents ranging from antidepressants to antiasthmatic and anti-inflammatory agents.

CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)0 = adenosine 5'-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                               MEDLINE=94019330; PubMed=8413254;
Bolger G., Michaeli T., Martins T., St John T., Steiner B.,
Rodgers L., Riggs M., Wigler M., Ferguson K.;
"A family of human phosphodiesterases homologous to the dunce learning and memory gene product of Drosophila melanogaster are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005626; C:insoluble fraction; TAS.
GO:0005625; C:soluble fraction; TAS.
GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93203241; PubMed-8384210;
McLaughlin M.M., Cieslinski L.B., Burman M., Torphy T.J.,
Livi G.P.;
                                                                                                                                                                                                                                                                                                          Electron, J. 328:549-558(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biochemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                   UENCE FROM N.A. (ISOFORMS PDE4B1 AND PDE4B2)
                                                                                                                                                                           potential targets for antidepressant drugs.";
Mol. Cell. Biol. 13:6558-6571(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A low-Km, rolipram-sensitive, cAMP-specific human brain. Cloning and expression of cDNA, characterization of recombinant protein, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- ENZYME REGULATION: Inhibited by rollipram.
-1- PATHWAY: Cyclic nucleotide metabolism.
-1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q07343-2; Sequence=VSP_004572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q07343-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM PDE4B2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chem. 268:6470-6476(1993)
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MEDLINE=95145731; PubMed=7843419;
           59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | : | :: | :: | :: | :: | 311 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 MYAIFQERDLLKTFRISSDTFIITYMMTLEDHYHSDVAYHNSLHAADVAQSTHVILSTPAL 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKIL 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        548 NYTDRIQVLRNMVHGADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 607
                                                                                                                           splicing; Multigene family; 3D-structure. MKGSRSWHWADDNVKDYENCSLSKÄYKSSRNHLGIDLWR GRRCCSGNLGLPESOROSEBARTPEGOGISRPTTLELTT. PSIAITIVSQE -> MTAKOSSKELTASEPEVCIKTFKEGM
                                                                                                                                                                                                                                                                                                                                                       IVTPPAQVLASLRSVENNFTILTNLHGTSNKRSPAASQPPV
SRVNPQ -> MKKEHGGIFSSTGISGGSGDSAMDSLQPLQP
NYMPVCLFA (in isoform PDE4B2).
                                                                                                                                                                                                                                                                          MKKSRSVMTVMADDNVKDYFECSLSKSYSSSSNTLGIDLWR
GRRCCSGNLQLPPLSQRQSERARTPEGDGISRPTTLPLTTL
                                                                                                                                                                                                            HLELELPRLPGURPTSPKISPRSSPRNSPCFFRKLLVNKSI
RORRRFTVAHT (in isoform PDE4B3).
                                                                                                                                                                                                                                                                                                                    PSIAITTVSQECFDVENGPSPGRSPLDPQASSSAGLVLHAT
                                                                                                                                                                                                                                                                                                                                          FPGHSQRRESFLYRSDSDYDLSPKAMSRNSSLPSEQHGDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 ANSVIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN4C_HUMAN STANDARD, PRT; 712 AA.

Q08433; Q9UN44; Q9UN45; Q9UN56; Q9UPG6,
01-007-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last amnotation update)
cAMP-specific 3',5'-cyclic phosphodiesterase 4C (BC 3.1.4.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.5%; Score 550; DB 1; Length 736; 31.8%; Pred. No. 2.3e-37; ive 84; Mismatches 152; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR--
                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP 004572.
208FCE9CD40EF5EB CRC64;
                                                                                                                                                                                                                                                        004571.
                                                                                                                                                                                                                                                        /FTId=VSP
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InterPro; IPR003607; Met phsphohydro.
InterPro; IPR002073; PDEase.
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                   InterPro; IPR002073; PDESSE.
Pfam; PF00233; PDESSE; 1.
PRINTS; PR00387; PDIESTERASE1.
SWART; SMO6471; HDC; 1.
PROSITE; PS00126; PDEASE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               736 AA; 83343 MW;
                                                                                                                         Hydrolase; cAMP; Alternative VARSPLIC 1 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                            211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DPDE1) (PDE21).
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                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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CN4C HUMAN
CN4C HUMAN
AC 008493,
DT 21-0CT-
DT 22-0CT-
DB CAMP-sp
DB CAMP-sp
DB CAMP-sp
CO ENEXAL
CO ENEXA
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SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ranirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,

Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,

Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,

Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,

Kronmiller B., Arellano A., Saunders C., Ow D., Nolan M., Trong S.,

"Sobayashi A., Olsen A.S., Carrano A.V.;

"Sequence analysis of an ~600 kb region in 19p13.1 between JAK3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94019330; PubMed=8413254;
Bodger G., Michaeli T., Martins T., St John T., Steiner B.,
Rodgers L., Riggs M., Wigler M., Ferguson K.;
"A family of human phosphodisesterases homologous to the dunce
learning and memory gene product of prosophila melanogaster are
potential targets for antidepressant drugs.";
Mol. Cell. Biol. 13:6558-6571 (1993).
-!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O
                                                                                                                                                                                                                                                                                                                                                      to
                                               human
                                                                                                                                                                                                                                                       Sullivan M., Olsen A.S., Houslay M.D., "Genomic organisation of the human cyclic AMP-specific phosphodiesterase PDE4C gene and its chromosomal localisation (1913.1, between RaB3A and JUND."; Cell. Signal. 11:735-742(1999).
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                                                                                                                                                   [2] SEQUENCE FROM N.A. (ISOFORMS PDE4C1; PDE4C2 AND PDE4C3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
Engels P., Sullivan M., Mueller T., Luebbert H.; "Molecular cloning and functional expression in yeast CAMP-specific phosphodiesterase subtype (PDE IV-C)."; FEBS Lett. 358:305-310(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q08493-4; Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q08493-6; Sequence=Not described;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=008493-2; Sequence=VSP_004575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adenosine 5'-phosphate.
--- ENZYME REGILATION: Inhibited by rolipi
---- PATHWAY: Cyclic nucleotide metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q08493-1; Sequence=Displayed;
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EMBL, AF157811; AAD47053.1; JOINED.
EMBL; AR157814; AAD47053.1; JOINED.
EMBL; AR157815; AAD47053.1; JOINED.
                                                                                                                                                                                                                               MEDLINE=20039485; PubMed=10574328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 462-712 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=PDE4C3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=PDE4C5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=PDE4C6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=PDE4C7
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TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I-----LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 HLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 QIPADTLATYLLMLEGHYHANVAYHNSLHAADVAQSTHVLLATPALEAVFTDLEILAALF 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CADICNPCRIWELSKOMSEKVTEEFFHQGDIBKKYHLGVSPLCDRHTESIANIQIGFMTY 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                             PRINTS; PROGRAT; PDIEGEBRASEL.
SMART; SMO0471; HDC; 1.
PROSITE; PSO0126; PDEASE_I; 1.
Hydrolase; cAMP; Multigene family; Alternative splicing; 3D-structure.
VARSPLIC.
                                                                                                                                                                                                                                                                                   IQQRFYSDPDKSAGCRERDLSPRPELRKSRLSWPYSSCRR
-> MQGPPAPAPVPGPGSPRGSPRGSPGLFRKLLVNQSIRL
QRRFTVAHPLC (in isoform PDE4C3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 SATVPREGVQIDQEEQLAKELEDTNKWGLDVFKVAELSGNRPLTAIIFSIFQERDLLKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 AAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESG--LFSHLPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRQQMETQIGALILATDISRQNEYLSLFRSHLDR-----GDLCLEDTRHRHLVLQMALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 ESERRGSH--PYIDFRIFHSQSEIEV-SVSARNIRRLLSFQRYLRSSRFFRGTAVSNSLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                          MIM; v00128; -.
GG; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
InterPro; IPR003007; Met_phsphohydro.
InterPro; IPR002073; PDEase.
Pfam; PF00233; PDEase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.3%; Score 545; DB 1; Length 712; 33.8%; Pred. No. 5.6e-37; ive 68; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                     /FTId=VSP 004574.
Missing (in isoform PDE4C2).
/FTId=VSP 004575.
K -> N (IN REF. 2).
D -> Y (IN REF. 2).
EL -> DV (IN REF. 1).
NSE -> K (IN REF. 1).
KF -> D (IN REF. 1).
          AF157812; AAD47054 1; JOINED.
AF157814; AAD47054 1; JOINED.
AF157815; AAD47055 1; JOINED.
AF157816; AAD47055 1; JOINED.
AF157816; AAD47055 1; JOINED.
AF157815; AAD47055 1; JOINED.
AC005759; AAC83047 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           79901 MW;
                                                                                                    L20968; AAA03591.1;
                                                                                                                        LXU; 26-JUN-02.
HGNC:8782; PDE4C.
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604 IAHPLWETWA 613
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340
446
447
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                                                                                                            PIR; S71626; S71626
PDB; 1LXU; 26-JUN-02
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339
344
444
446
712 AA;
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Matches 12
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EMBL;
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809 AA.

CN4D HUMAN STANDARD; PRT; 809 Q08499; O43433; Q13549; Q13550; Q13551; 01-OCT-1996 (Rel. 34, Created)

RESULT 11 CN4D_HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=4; Synonyms=hpDE4DL;
Iso1d=Q06499-4; Sequence=VSP_004579;
Name=5; Synonyms=hpDE4DL;
Iso1d=Q08499-5; Sequence=VSP_004580;
Name=6; Synonyms=hpDE4D5;
Name=6; Synonyms=hpDE4D5;
Iso1d=Q08499-6; Sequence=VSP_004576;
TISSUE SPECIFICITY: WIDESPERAD; MOST ABUNDANT IN SKELETAL MUSCLE.
SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIANE=94171048; PubMed=8125310;
Baecker P.A., Obernolte R., Bach C., Yee C., Shelton E.R.;
"Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP
phosphodiesterase (PDE IVD).";
                                                                                                                                                                                                                                                                                                                                                                                                     ဥ
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-!- CATALYRIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O adenosine 5'-phosphate.
-!- RAZEMENTION: Inhibited by rolipram.
-!- PATHWAY: Cyclic muclocide metabolism.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6), AND REVISIONS
                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=44019330; PubMed=8413254;
Belger G., Michaeli T., Martins T., John T., Steiner B.,
Rodgers L., Riggs M., Wigler M., Ferguson K.;
"A family of human phosphodiesterases homologous to the dunce learning and memory gene product of Drosophila melanogaster are potential targets for antidepressant drugs.";
Mol. Cell. Biol. 13:6558-6571(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
c 3',5'-cyclic phosphodiesterase 4D (EC 3.1.4.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98041897; PubMed=9371713;
Bolger G. B., Erdogan S., Jones R.E., Loughney K., Scotland Hoffmann R., Wilkinson I., Farrell C., Houslay M.D.;
"Characterization of five different proteins produced by alternatively spliced mRNAs from the human cAMP-specific phochaelesterase PDE4D gene.";
Biochem. J. 3281539-548 (1997).
                                                                                                                                                Catarrhin; Hominidae; Homo.
                                                                                Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
(1011_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=6;
Name=1; Synonyms=hPDE4D4;
Isola=0208499-1; Squence=Displayed;
Name=2; Synonyms=hPDE4D3;
Isola=208499-2; Sequence=VSP_004577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q08499-3; Sequence=VSP_004578;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 138:253-256(1994)
                                     CAMP-specific 3' (DPDE3) (PDE43).
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288 LEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCD 347
                                                                                                   542 ILQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMVETKKVTSSGVLL 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Livi G.P., Kmetz'P., McHale M.M., Cieslinski L.B., Sathe G.M., Taylor D.P., Davis R.L., Torphy T.J., Balcarek J.M.; "Cloning and expression of cDNA for a human low-Km, rolipram-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sullivan M., Rena G., Begg F., Gordon L., Olsen A.S., Houslay M.D.; "Identification and characterization of the human homologue of the short pDE4A cAMP-specific phosphodiesterase RD1 (PDE4A1) by analysis of the human HSPDE4A gene locus located at chromosome 19p13.2."; Biochem. J. 333:693-703(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             learning and memory gene product of Drosophila melanogaster are potential targets for antidepressant drugs."; Mol. Cell. Biol. 13:6558-6571(1993).
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"Molecular cloning of a novel splice variant of human type IVA (PDE-IVA) cyclic AMP phosphodiesterase and localization of the to the pl3.2-q12 region of human chromosome 19.";

Biochem. J. 308:683-691(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94019330; PubMed=8413254;
Bolger G., Michaeli T., Martins T., St John T., Steiner B.,
Rodgers L., Riggs M., Miglar M., Ferguson K.;
"A family of human phosphodiesterases homologous to the dunce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EC 3.1.4.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                                                        P27815, 075522, 076092; Q16255; Q16691; Q8WUQ3; 01-AUG-1992 (Rel. 23, Created) 01-007-1996 (Rel. 34, Last sequence update) 10-007-2003 (Rel. 42, Last annotation update) cAMP-specific 3',5'-cyclic phosphodiesterase 4A
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                                                                                                                                                                                                                                                                                                                                                                      886 AA
                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 3 AND 5).
                                                                                                                                                                             348 RHTESIANIQIGFMTYLVEPLFTEWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Cell. Biol. 10:2678-2686(1990)
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MEDLINE=90258854; PubMed=2160582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEV-----SVSARNIRRLLSFQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VSP_004576.
MRARGGSAPAGGGEGSAGGATLKAPKHLWRHEQHHQY
PLRQPGFLLHPHLLPPPPPSPQPQPQCELQPPPPPLP
PPPPPPGAAKGRYASSGATGRVRHGYSDTERYLYCRAMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSYAVETGHRPGLKKSRMSMPSSFQGLRRFDVDNGFGAGRS
PLDPMTSPGSGLILQANFVHSQRRESFLYRSDSDYDLSPKS
MSRNSSIASDIHGDDLIVTPFAQVLASLRTVRNNFAALTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLRQPQFRLLHPHHLPPPPPSPQPQPQCPLQPPPPPPP
PPPPPPGAARGRYASSGATGRVRHRGYSDTERYLYCRAMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VSP_004578.
MEAEGSSAPARAGSGEGSDSAGGATLKAPKHLWRHEQHHQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLRQPQFRLLHPHHILPPPPPSPQPQPQCPLQPPPPPPLP
PPPPPGAARGRYASSGATGRVRHRGYSDTERYLYCRAMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          splicing; Multigene family; 3D-structure. MEAEGSSAPARAGSGEGSDSAGGATLKAPKHLWRHEQHHQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSYAVETGHRPGLKKSRMSWPSSFQGLRR -> MAQQTSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISYAVETGHRPGLKKSRMSWPSSFQGLRR -> MMHVNNFF
                                                                                                                                                                                                                                                                                       MIM; 600129; -. Ginsoluble fraction; TAS. GO; GO:0005625; C:insoluble fraction; TAS. GO; 00016625; C:soluble fraction; TAS. GO; 0004115; F:cAMP-specific phosphodiesterase activity; TAS. InterPro; IPR003607; Met_phsphohydro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDRAPSKRSPMCNQPSINKATIT -> MKEQ
AGYGRMAPFELASGPVKRLRTESPFPCLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7A4773DD3A044F57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRHSWIC (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP 004580.
R -> P (IN REF. 3).
C -> R (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.2%; Score 542; DB 1; 31.6%; Pred. No. 1.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (in isoform 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isoform 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTIG=VSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing
1220970; AAA03592.1; -...
1220969; AACC0042.1; -...
1002882; AACC13745.1; -...
1050157; AAA97890.1; -...
1050159; AAA97891.1; -...
1050159; AAA97891.1; -...
1050159; AAA97891.1; -...
1050159; AAA07892.1; -...
1050159; AACC00070.1; -...
1050159; AACC00069.1; -...
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PRINTS, PR00387, PDIESTERASE1.
SMART; SM00471, HDc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00126; PDEASE I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; cAMP; Alternative VARSPLIC 1 152
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                                                                                                                                                                                                               PDB; 1MKD; 01-MAR-03.
Genew; HGNC:8783; PDE4D.
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769
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769
809 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 600129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122;
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EMBL;
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Matches
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DP GA

95 AG

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U68532; AAC63832.1;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                              TASULEMENTALIA,

RAY

MEDDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altasner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Brachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brachenko L., Waller R.B., Bonaldow M.F., Carainci P., Prange C.,

RA Bask S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boask S.A., McWan P.J., McKernan K.J., Malek J.A., Gunzarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Shevohenko Y., Bouffard G.G.,

RA Bakesley R.W., Young A.C., Schwutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RH Human and mouse CDNR sequences.";

RT Human and mouse CDNR sequences.";

RC -! CATAINTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =

adenosine S'-phosphate.

CC -! CATAINTIC ACTIVITY: Inhibited by rolipram.

CC -! ENZYME REGILATION: Inhibited by rolipram.

With momband mouse CDNR sequences.";

-! CATAINTARS.

CC -! PATHWAY: Cyclic nucleotide metabolism.

CC -! DATHWAY: Cyclic nucleotide metabolism.

CC -! PATHWAY: Machanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=2; Synonyms=TM3;
IsoId=P27815-2; Sequence=VSP 004556;
Name=3; Synonyms=PDE4A7, PDE4A6;
IsoId=P27815-3; Sequence=VSP 004557;
Name=4; Synonyms=PDE4A1, RD1;
IsoId=P27815-4; Sequence=VSP 004559;
Name=5; Synonyms=PDE4A8, ZE1;
IsoId=P27815-5; Sequence=VSP 004559, VSP 004561;
Note=Probably represents a non-functional splice variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bvent=Alternative splicing; Named isoforms=5;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1; Synonyms=PDE46;
IsoId=P27815-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L20965; AAA03588.1; -. AR669491; AAC35012.1; -. AR669489; AAC35012.1; JOINED. AR669489; AAC35012.1; JOINED. AR669489; AAC35012.1; JOINED. AR669489; AAC35013.1; JOINED. AR669489; AAC35013.1; JOINED. AR669489; AAC35013.1; JOINED. AR669489; AAC35014.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF069491; AAC35015.1;
AF069488; AAC35015.1; JOINED.
AF069489; AAC35015.1; JOINED.
AF069490; AAC35015.1; JOINED.
FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M37744; AAA69697.1;
U18087; AAC50458.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U18088; AAA98540.1
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EMBL;
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EMSRSGNQVSEYISTTFLDXQNEVEIPSPTMKEREKQQAPRPRPSQPPPPVPHLQPMSQ 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 ITGLKKCMHSNSLNNSNIPRFGVKTDQEELLAQELENLNKWGLNIFCVSDYAGGRSLTCI 394
                                                                                                                                                                                                                                                                                                                                                                                              KIQQRGYSDSAERAERERQPHRPIERADAMDTSDRPGLRTT
RMSWPSSFHGTGSGSGGGSSRR -> MARPRGLGRIPE
LQLVAFPVAVAAEDEAFLPEPLAPRAPRRPRSPFSSPVFFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7.T.d=VSP 004556.
MEPPTVPSERSLSLSLPGPREGQATLKPPPQHLWRQPRTPI
RIQORGYSDSAERARRERQHRPIERADAMOTSDRPGLRTT
RIAMPSSFRPGTGTGGGGGGGSRRFEABENGPTPSPGRSPL
DSQASPGLVHAGAATSQRRESFLYRRDSDYDNSPKTWRSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           riqorgysdsaeraererophrpieradamotsdrpclrtt
rmswpssfhgtgtgsggagggssrrfeaengptpspgrspl
dsqaspglvlhagaatsqrresflyrsdsdydmspktmsrn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSVTSEAHAEDLIVTPFAQVLASLRSVRSNFSLLTNVPVPS
NKRSPLGGPTPVCKATLSEETCQQLARETLEELDWCLEQLE
TWQTYRSVSEMASHK -> MPLVDFFCETCSKPWLVGWWDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMSWPSSFHGTGTGSGGAGGSSRRFEAENGPTPSPGRSPL
DSQASPGLVLHAGAATSQRRESFLYRSDSDYDMSPKTMSRN
SSVTSEAHAEDLIVTPFAQVLASLRSVRSNFSLLTNVPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVTSEAHAEDLIVTPFÄQVLASLRSVRSNFSLLTNVPVPS
NKRS -> MCPFPVTTV (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP 004558.
MEPPTVPSERSLSLSLPGPREGQATLKPPPQHLWRQPRTFI
RIQQRGYSDSAERAERERQPHRPIERADAMDTSDRPGLRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKRSPLGGPTPVCKATLSEETCQQLARETLEELDWCLEQLE
TMQTYRSVSEMASHKFKRMLNRELTHLSEMSRSGNQVSEYI
                                                                                                                                                                                                                                                                                                                                                       splicing; Multigene family.
MEPPTVPSERSLSLSGPREGQATLKPPPQHLWRQPRTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STTFLDKQNEVEIPSPTMKEREKQQAPRPRPSQPPPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform 5).
/FTrd=VSP 004561.
= > A (IN REF. 1, 2, 6; AAB33798 AND 7).
#493BDF99BBA9756CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>MEPPTVPSERSLSLSLPGPREGQATLKPPPQHLWRQPRTPI</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOPMSQITGLKKLMHSNSLNNSNIPRFGVKTDQEBLLAQ
-> MVLPSDQGFKLLGNVLQGPBPYRLLTSGLRLHQ (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPSPTFRRIRLRLLRSCODLGRQAWAGAG (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Gaps
                                                                                             /FTId=VSP_004559.
GFIDYIVHPLWETW -> QARGIDGRAQGGFY (in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 1.6e-36;
69; Mismatches 159; Indels
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Pred. No. 1.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'FTIG=VSP 004557.
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/FTId=VSP 004560.
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FTId=VSP 0045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98201 MW;
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U97584; AAC25679.1; -. BC019864; AAH19864.1;
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                                       PIR; A54442; A54442.
PIR; S55348; S55348.
Genew; HGNC:8780; PDE4A.
MIM; 600126; -.
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                                             RESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD-----RGDLCLE
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                                                                                                178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Monaco L., Vicini E., Conti M.;
Monaco L., Vicini E., Conti M.;
"Structure of two rat genes coding for closely related rolipram-
sensitive cAMP phosphodiesterases. Multiple mRNA variants originate
from alternative splicing and multiple start sites.";
J. Biol. Chem. 269:347-357(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGURNCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=94308045; PubMed=8034568;
Sette C., Vicini E., Conti M.;
"The ratPDE3/IVd phosphodiesterase gene codes for multiple proteins differentially activated by CAMP-dependent protein kinase.";
J. Biol. Chem. 269:18271-18274(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bolger G.B., Rodgers L., Riggs M.; "Differential CNS expression of alternative mRNA isoforms of the mammalian genes encoding cAMP-specific phosphodiesterases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90046763; PubMed=2554303;
Swinnen J.V., Joseph D.R., Conti M.;
"The mRNA encoding a high-affinity cAMP phosphodiesterase is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EC 3.1.4.17)
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
cAMP-specific 3',5'-cyclic phosphodiesterase 4D (DPDE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           672 AA
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SEQUENCE OF 95-672 FROM N.A. (ISOFORM 1).
MEDLINE=95047482; PubMed=7958996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monaco L., Vicini E., Conti M.,
J. Biol. Chem. 269:20806-20806(1994).
                                                                                                                                                                                                                                                                                                                                                              | |: |:||: |:| ||: || TASVEKSQVGFIDYIVHPLWETWA 658
                                                                                                                                                                                                                                                                                                                                      TESIANIQIGEMTYLVEPLFTEWA 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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REVISION TO 6.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMHVNTFPFRRHSWICFDVDNGTSAGRSPLDPMTSPGSGLI
LQANFVHSQRRESFIYRSDSDYDLSPKSMSRNSSIASDIHG
DDLIVTPFRAQVLASLRTVRNNFAALTNLODRAPSKRSPMCN
QPSINKATIT -> MKEQPSCAGTGHPSWAGYGRNAPFELA
GGPVKRLRTESPFPCLFA (in isoform 2)
/FTId=VSP_004581.
                                                                                                     phosphorylation. SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
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Hydrolase; cAMP; Alternative splicing; Multigene family;
                                                                                                                                                                                                                                                                                                                                                           Isoid=P14270-2; Sequence=VSP_004581;
Name=3; Synonyms=PDE3.2;
Isoid=P4270-3; Sequence=VSP_004582;
PTM: IsoeForm 1 is rapidly activated by PKA through
                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3;
Name=1, Synonyms=PDE3.3;
IsoId=P14270-1; Sequence=Displayed;
Name=2; Synonyms=PDE3.1;
regulated by hormones and CAMP.";
Proc. Natl. Acad. Sci. U.S.A. 86:8197-8201(1989).
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InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; U01283; AAA18924.1; JOINED.
; U01284; AAA18924.1; JOINED.
; U01285; AAA18924.1; JOINED.
; U01286; AAA18924.1; JOINED.
; U01287; AAA18924.1; JOINED.
; U01279; AAA18924.1; JOINED.
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SMART; SM00471; HDc; 1.
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                                                            SEQUENCE OF 224-672 FROM N.A.
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AAA18925.1;
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U09455; AAA20401.1;
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U01287; J
U01279; J
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U01284;
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PATHWAY: Cyclic nucleotide metabolism.
SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
family.
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32.2%; Pred. No. 2.8e-36;
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FIR, 167945; IF67945.
InterPro; IPR003607; Met_phsphohydro.
InterPro; IPR02073; PDEase.
Ffan; PF00237; PDEase.
FRINTS; PR00387; PDESTERASE1.
SMART; SM00471; HDC; 1.
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Hydrolase; cAMP; Multigene family.
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                                                                                                                                                                                                                                                                      EMBL; L27061; AAA56858.1; -.
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Best Local Similarity 32.2
Matches 118; Conservative
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507 5
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                  RYLRSSRFFRGTAVSNS----LNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLV 115
                                                                                                                                                                                                                                                                                                                                                                                                   285
                                                                                                                                                                                                                                                                                                                                                                                                                                            SLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 KLANSVIPWDILLISLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSBLALMYNDSSVLENHHLAVGFK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD-----RGDLC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 LEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCD 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 VIMHTIFQERDILKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAADVVQSTHVLLSTP
                                                                                                                                                                                                                                                                                                                                                                                                   KLMHSS-----SLTNSCIPRFGVKTEQEDVLAK-ELEDVNKWGLHVFRIAELSGNRPLT
                                                                                                                                                                                                                                                                          ----SVSARNIRRLLSFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swinnen J.V., Joseph D.R., Conti M.;
"Molecular caloning of rat homologues of the Drosophila melanogaster aduce cAMP phosphodiesterase: evidence for a family of genes.";
proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
-!- CATALYTIT ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)0 = adenosine 5'-phosphate.
-!- ENZYME REGULATION: Inhibited by rolipram.
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DALLE ENTIAL CNS expression of alternative mRNA isoforms of mammalian genes encoding cAMP-specific phosphodiesterases."; Gene 149:237-244(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EC 3.1.4.17)
                                                                                                                                                                                             Length 672;
                                                                                                                                                                                                                                  81; Mismatches 151; Indels
                         Missing (in isoform 3).
/FIGL=VSR 004582.
A - N (IN REF. 3).
MISSING (IN REF. 4).
G - > E (IN REF. 3).
C - Y (IN REF. 3).
W, 63CE38PA654A0BDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR 1990 (Rel. 14, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
cAMP FSPE-2003 (Sel. 41, Last annotation update)
                                                                                                                                                                                                                                                                          RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEV-
                                                                                                                                                                                         Score 539; DB 1;
Pred. No. 1.6e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=95047482; PubMed=7958996;
                                                                  95 A
355 MI
510 G
626 C
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                                                                                                                                                                                           24.0%;
31.6%;
                                                                                                                                                                                                                                    Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                              167
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                                                                                                                               626
672 AA;
                                                                                                                                                                                                              Similarity
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                                                                  CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                             Query Match
                              VARSPLIC
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CN4C_RAT

CN4C_RAT

CN4C_RAT

D1 01-A

D1 01-A

D1 01-A

D2 01-A

D3 01-A

D4 01-A

D5 01-A

D6 01-A

D7 01-A

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D8 01-A

D9 01-A

D9 01-A

D1 01-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 NSINILDDDYNGQAKCMLEKVGNWNFDIFLFDRLFNGNSLVSLTFHLFSLHGLIEYFHLD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 PRFGVQTDQEEQLAK-ELEDTNKWGLDVFKVAELSGNRPLTAVIFRVLQERDLLKTFQIP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ESERRGSH--PYIDFRIFHSQSEIEVSVSARN----IRRLLSFQRYLRSSRFFRGTAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 ETSRSGNQVSEYISQTFLDQQAEVELPAPPTEDHPWPMAQITGLRKSCHTS---LPTAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 QMETQIGALILATDISRQNEYLSLFRSHLDR-----GDLCLEDTRHRHLVLQMALKCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 MMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAA
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OGOGÉB; Q96911; Q96PD0; Q96PD0; Q96PD1; Q9UMB7;
15-UUL-1999 (Rel. 38, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
High-affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A (EC 3.1.4.17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R -> S (IN REF. 2).
S -> N (IN REF. 2).
87D12BE2C46642F3 CRC64;
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Search completed: May 26, 2004, 09:25:02 Job time : 19 secs 셤 ð 쉽 셤 9 à à 셤 8 g ਨੇ ò à This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Carim L., Estivill X., Sumoy L., Escarceller M.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Plays a role in signal transduction by regulating the intracellular concentration of cyclic nuclectides. This phosphodiesterase, which has a high affinity for CAMP, may be involved in maintaining basal levels of the cyclic nuclectide and/or in the CAMP regulation of germ cell development.

-!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)0 = adenosine 5'-phosphate.

-!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)0 = cyclic nuclectide and/or in the cAMP regulation of germ cell development.

-!- COFACTOR: Requires divalent cations. Magnesium or manganese are required for maximum activity, in vitro.

-!- ENEXME REGULATION: Inhibited by dipyridimole. Insensitive to as lot the non-selective including rollpram and zaprinast as well as to the non-selective inhibitor, IBMX. Unaffected by GMP. small intestine and colon. DOMAIN: Composed of a C-terminal catalytic domain containing two putative divalent metal sites and an N-terminal regulatory domain. SEQUENCE OF 117-829 FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE-98289571; PubMed-9618352;
Fisher D.A., Smith J.F., Pillar J.S., St Denis S.H., Cheng J.B.;
"Isolation and characterization of PDE8A, a novel human cAMP-specific Name=2; Synonyms=PDEBA2;
Isod=06658-2; Sequence=VSP_004597;
Name=3; Synonyms=PDEBA3;
Isod=066658-3; Sequence=VSP_004596;
Name=4-5; Synonyms=PDEBA4, PDEBA5;
Isod=066658-4; Sequence=VSP_004595;
ISOJ=066658-4; Sequence=VSP_004595;
ISSUE SPECIFICITY: Expressed in most tissues except thymus and peripheral blood Leukocytes. Highest levels in testis, ovary, SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase -!- SIMILÂRITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain. -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain. TISSUE=Testis;
MEDDINE=21601118; PubMed=11738832;
Wang P., Wu P., Egan R.W., Billah M.M.;
Human phosphodiesterase 8A splice variants: cloning, gene organization, and tissue distribution.";
Gene 280:183-194(2001). Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Event=Alternative splicing; Named isoforms=4; Name=1, Synonyms=PDE8A1; IsoId=0600658-1; Sequence=Displayed; Biochem Biophys. Res. Commun. 246:570-577(1998) SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4-5) EMBL, AF388183; AAL18610.1; -EMBL, AF388184; AAL18611.1; -EMBL, AF388185; AAL18612.1; -EMBL, AF388187; AAL18613.1; -EMBL, AF389187; AAL18614.1; -EMBL, AF056490; AAC19763.1; -EMBL; AL109687; CAB52020.1; --SEQUENCE OF 670-829 FROM N.A. ALTERNATIVĖ PRODUCTS: JW0088; JW0088. phosphodiesterase. NCBI_TaxID=9606;

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54 RILISPORYLRSSRFFRGTAVSNSLNILD----DDYNGQAKCMLEKVGNWNFDIFLFDRLT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510 HNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIEANYHSSNPYHNSTHSADVLHATA 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 CLEDT-------RHRHLVLQMALKCADICNPCRIWELSKQWSEKVTBEFF 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690 TLEENGETDKKQEVINTMLRTPENRTLIKRMLIKCADVSNPCRPLQYCIEWAARISEEYF 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 HQGDIEKKYHLG-VSPLCDRHTESIANIQIGFMTYLVEPLFTEWARFSNTRLSQTMLGHV 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750 SQIDBEKQQGLPVVMPVFDRNICSIPKSQISFIDYFIIDMFDAMDAFVDL---PDLMQHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454 RRLSGNEYVLST---KNTQMVSS-NIITPISLDDVPPRIARAMENEEYWDFDIFELEAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Gaps
                                                                                                                                                                                                                                                                                                                                              CATALYTIC (BY SIMILARITY).
MAGNESIUM OR MANGANESE 1 (POTENTIAL).
MAGNESIUM OR MANGANESE 1 (POTENTIAL).
MAGNESIUM OR MANGANESE 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                            TIGRFAMS; TIGR00229; sensory_box; 1.
PROSITE; PS00126; PDRASE_I; 1.
PROSITE; PS50112; PAS; I.
Hydrolase; cAMP; Alternative splicing; Manganese; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.4%; Score 503; DB 1; Length 829
31.6%; Pred. No. 1.9e-33;
Live 76; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93303 MW; 99BD05EA185A42CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform 4-5)
/FTIG=VSP 004595.
Missing in isoform 3).
/FTIG=VSP 004596.
Missing (in isoform 2).
/FTIG=VSP_004597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoform 4-5)
GO; GO:0009187; P:cyclic nucleotide metabolism; NAS.
InterPro; IPR003607; Met_phsphohydro.
InterPro; IPR00014; PAS domain.
InterPro; IPR000014; PDEase.
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I -> V (IN REF. 2)
                                                                                                                                                                                                                                                                                                                              PAC.
CATALYTIC
                                                                             Pfam; PF00289; PAS; 1.
Pfam; PF00233; PDEase; 1.
PRINS; PR00387; PDIESTERASE1.
SWART; SW00471; HDC; 1.
SWART; SW00091; PAS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                   Multigene family.
DOMAIN 213
DOMAIN 287
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5560
560
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Sequence 2, Appli
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Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 120, App
Sequence 120, App
Sequence 120, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                       May 26, 2004, 09:26:43 ; Search time 577 Seconds (without alignments) 205.928 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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1 DQTALYIRMLGDVRVRSRAG......DTDAAFELNSQILPQENRLS
GenCore version 5.1.6
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US-09-989-442-120

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ALIGNMENTS

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RESULT 1 US-09-966-781A-1 US-09-966-781A-1 Sequence 1, Application US/09966781A Publication No. US20030036184A1 GENERAL INFORMATION: APPLICANT: SOULARN: TITLE OF INVENTION: SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY FILE REPRENCE: AD000281US CURRENT APPLICATION NUMBER: US/09/966,781A CURRENT FILING DATE: 2001-09-28 FRIOR FILING DATE: 2000-09-28 NUMBER OF SEQ ID NOS: 35 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1 LENGTH: 426 TYPE: PAT TYPE: PAT CORCANISK: Home sapiens US-09-966-781A-1	Query Match 100.0%; Score 2243; DB 10; Length 426; Best Local Similarity 100.0%; Pred. No. 3.1e-225; Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps	QY 1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRELLSFQR 6 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRELLSFQR 6	OY 61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLFNGNSLVSLTFH 1:	QY 121 LFSLHGLIEYFHLDWKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMFCYLKEPKLANS 1 Db 121 LFSLHGLIEYFHLDWKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 1	Qy 181 VTFWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 2

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GENERAL INFORMATION:

Sequence 2, Application US/09966781A

Sequence 2, Application US/09966781A

Publication No. US20030036184A1

GENERAL INFORMATION:

TITLE OF INVENTION: SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY

TITLE OF INVENTION: SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY

FILE REFERENCE: A0000281US

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: US/09/966,781A

PRIOR PILING DATE: 2000-09-28

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 426
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PUZOI.
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
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93.7%; Pred. No. 8.2e-211;
tive 13; Mismatches 14;
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Best Local Similarity 93.77
Matches 399; Conservative
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Sequence 3, Application US/09966781A

Publication No. US20030036184A1

GENERAL INFORMATION:

TITLE OF INVENTION: PALYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR TITLE OF INVENTION: SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY CURRENT APPLICATION NUMBER: US/09/966,781A

CURRENT APPLICATION NUMBER: US/09/966,781A
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Pred. No. 5.8e-212;
9; Mismatches 16;
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PRIOR FILING DATE: 2000-09-28
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SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Rattus sp.
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Matches 401; Conserv
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US-09-966-781A-3
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71 TAVSNSLNILDDDYNGOAKCMLEKVGNWNFDIFLFDRLINGNSLVSLTFHLFSLHGLIBY 130
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                                                                                                                                                271 NEYLSLFRSHLDRGDLCLEDTRHRHIVLQMALKCADICNPCRIWELSKQWSEKVTEEFFH 330
                                                                                                                                                                                                                                     331 QGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFTEWARFSNTRLSQTMLGHVGL 390
                                                                                                                                                                                                                                                                241 QGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVBPLFTEWARFSNTRLSQTMLGHVGL 300
61 SQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIK 120
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                                                                                         121 TNHYLATLYKNISVLENHHWRSAVGLIRESGLFSHLPLESRQQMETQIGALILATDISRQ
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                                                                TNHYLATLYKNISVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQ
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OTHER INFORMATION: Incyte ID No. US20040054138A1 7476201CDI
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Best Local Similarity 62.9%; Pred. No. 2.6e-135;
Matches 253; Conservative 65; Mismatches 83;
                                                                                                                                                                                                                                                                                                                         NKASWKGLOREQSSSEDTDAAFELNSQLLPQENRLS 426
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PRIOR APPLICATION NUMBER: PCT/US01/20140
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/213,741
PRIOR APPLICATION NUMBER: 60/213,741
PRIOR PELING DATE: 2000-06-22
PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-07-14
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 8
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APPLICANT: LU, Yan
APPLICANT: Chavia. Narinder K.
TITLE OF INVENTION: PHOSPHODIESTERASES
FILE REPERRENCE: PI - 0.136 PCT
CURRENT APPLICATION NUMBER: US/10/311,104
CURRENT FILING DATE: 2002-12-12
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YAO, Monique G.
TRIBOULEY, Catherine M
LAL, Preeti G.
HAFALIA, April J. A.
BAUGHN, Mariah R.
FAMKUMAR, Jayalaxmi
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Publication No. US20040054138A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                                                                                                                                                             ; LOCATION: (419)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-208
                                                                                                                                                                                                                                                                                                                                                                                                       YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLINGNSLVSLTFH 120
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                                                                                                                                                                                                                                                                                            Length 432;
      Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 311 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 208
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Publication No. US20030138815A1;
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH;
TITLE OF INVENTION: New Phosphodiesterase type 7;
FILE REFERENCE: PDE7spliceFWRWS;
CURRENT APPLICATION NUMBER: US/10/258,746;
CURRENT FILING DATE: 2002-10-28;
NUMBER OF SEQ ID NOS: 4;
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                          Score 1903; DB 9;
Pred. No. 1.1e-189;
0; Mismatches 3;
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ilarity 99.2%;
Conservative
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US-10-258-746-2
                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 361; Conserv
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LENGTH: 336
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71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY 130
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          251 ROOMETOIGALILATDISRONEYLSLFRSHLDRGDLCLEDTRHRHLVLOWALKCADICNP
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APPLICANT: William James
APPLICANT: Cook, William James
APPLICANT: Cook, William James
APPLICANT: Mayers, Rachel E.
APPLICANT: Carroll, Joseph M.
APPLICANT: Carroll, WOVEL 27875, 22025, 27420, 17906, 16319,
TITLE OF INVENTION: DS092 AND 10218 MOLECULES AND USES THEREFOR
FILE REPERBENCE: WISTON NUMBER: 09/426, 282
PRIOR APPLICATION NUMBER: 09/426, 282
PRIOR FILING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-22
PRIOR PLILING DATE: 2000-01-25
PRIOR PLILING DATE: 2000-11-28
PRIOR PLILING DATE: 2001-10-31
PRIOR PLILING DATE: 2001-10-29
PRIOR PLILING DATE: 2001-02-9
PRIOR PLILING DATE: 2001-10-31
PRIOR PLILING DATE: 2001-10-31
PRIOR PLILING DATE: 2001-10-29
PRIOR PLILING DATE: 2001-12-07
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62.9%; Pred. No. 2.6e-135;
.ive 65; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                    371 EWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
                                                                                                                                                                                                                                                                                                                                                    440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPROHRSRGSSGS 481
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10386414 Publication No. US20040006016A1 GENERAL INFORMATION:
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Best Local Similarity 62.9
Matches 253; Conservative
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                                                                                                   191 IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLFLES 250
                                                                                                                                          260 IAAAAHDVDHPGVNQPFLIKTNHHIANLYQNMSVLENHHWRSTIGMLRESRLLAHIDRKEM 319
                                                                                                                                                                                                                                                                                 71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY
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Query Match
61.7%; Score 1383.5; DB 14; Length 502;
Best Local Similarity 62.9%; Pred. No. 2.6e-135;
Matches 253; Conservative 65; Mismatches 83; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030143588A1 7476201CD1
US-10-273-517-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 EWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 481
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US-10-273-517-1

US-10-273-517-1

Publication No. US20030143588A1

GENERAL INFORMATION:

APPLICANT: THORNATION:

APPLICANT: THORNATION, Michael B.; DING, Li

APPLICANT: TRIBOULEY, Catherine M.; LAL, Preeti G.

APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.

APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.

APPLICANT: RAMKUNGAR, Jayalaxmi; LU, Yan

APPLICANT: RAMKUNGAR, Jayalaxmi; LU, Yan

APPLICANT: RAMKUNGAR, JOSALOSE

FILE REFERENCE: PI-0136 USA

CURRENT APPLICATION NUMBER: 60/241,100

PRIOR FILING DATE: 2000-10-18

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-06-21

PRIOR PELING DATE: 2000-06-21

PRIOR FILING DATE: 2000-06-21

PRIOR PRI
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ORGANISM: Homo sapiens
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US-10-273-517-1
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CURRENT APPLICATION NUMBER: US/09/989,442
CURRENT FILING DATE: 2001-11-21
                  CURRENT FILING DATE: 2001-11-21
PRIOR PLING DATE: 2001-11-21
PRIOR PLING DATE: 2000-0-20
PRIOR PLING DATE: 2000-0-24
PRIOR PLING DATE: 2000-0-24
PRIOR PLING DATE: 2000-0-24
PRIOR PLING DATE: 2000-0-13
PRIOR PLING DATE: 2000-0-14
PRIOR APPLICATION NUMBER: 60/216, 86
PRIOR PLING DATE: 2000-0-14
PRIOR APPLICATION NUMBER: 60/216, 86
PRIOR PLING DATE: 2000-0-14
PRIOR PLING DATE: 2000-0-17
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-11-17
PRIOR PLING DATE: 2000-11-17
PRIOR PPLICATION NUMBER: 60/221, 36
PRIOR PLING DATE: 2000-11-17
PRIOR PPLICATION NUMBER: 60/221, 36
PRIOR PLING DATE: 2000-11-17
PRIOR PLING DATE: 2000-11-17
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PRIOR PLI
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FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/229,343
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                                    200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259
                                                                                                                   250
                                                                                                                                              320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379
                                                                                                                                                                                                                                                                                                                                                CRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFT 370
                                                                                                                                                                                                                                                                                                                                                                               380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFWSYIVEPLFR 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 YKWISVLENHHWRSAVGLIRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFR 121
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FHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLES
                                                                                                                                                                                                                                ROOMETOIGALILATDISRONEYLSLFRSHLDRGDLCLEDTRHRHLVLOMALKCADICNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 280, Application US/09764898
Patent No. US20020090673A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRESALS: PUZOI 100 NUMBER: US/09/764,898
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT APPLICATION NUMBER: US/09/164,898
CURRENT APPLICATION NUMBER: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 311
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 211;
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Publication No. US20030013649A1;
GENERAL INFORMATION:
APPLICANT: Rosen et al.,
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies;
FILE REFERENCE: PJZ08
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Best Local Similarity 98.1%; Pred. No. 4.7e-104;
Matches 202; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 HLGVSPLCDRHTESIANIQIGFMTYL 364
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
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US-09-989-442-120
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US-09-764-898-280
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LENGTH: 211
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NR APPLICATION NUMBER: 60/230,438

RETLING DATE: 2000-09-06

OR APPLICATION NUMBER: 60/215,135

RETLING DATE: 2000-06-30

RETLING DATE: 2000-08-14

OR APPLICATION NUMBER: 60/29,218

RETLING DATE: 2000-11-17

OR APPLICATION NUMBER: 60/249,218

RETLING DATE: 2000-11-17

OR APPLICATION NUMBER: 60/249,208

OR FILING DATE: 2000-11-17

OR APPLICATION NUMBER: 60/249,213

OR APPLICATION NUMBER: 60/249,213

OR APPLICATION NUMBER: 60/249,213
                                                                                                                                                                                                                                                                          R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/237,038
R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/236,370
R FILING DATE: 2000-09-29
R APPLICATION NUMBER: 60/236,802
R APPLICATION NUMBER: 60/236,802
R APPLICATION NUMBER: 60/237,037
R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/237,040
R FILING DATE: 2000-10-02
R FILING DATE: 2000-10-02
R FILING DATE: 2000-10-02
R FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/239,935
RR APPLICATION NUMBER: 60/239,935
RR FILING DATE: 2000-10-13
RR FILING DATE: 2000-10-13
RR FILING DATE: 2000-10-20
RR FILING DATE: 2000-10-20
RR APPLICATION NUMBER: 60/246,474
RR APPLICATION NUMBER: 60/246,532
RR FILING DATE: 2000-11-08
R FILING DATE: 2000-11-08
R FILING DATE: 2000-11-08
R FILING DATE: 2000-11-10
R FILING DATE: 2000-11-17
RR FILING DATE: 2000-11-17
RR FILING DATE: 2010-11-17
R FILING DATE: 2000-09-01

R APPLICATION NUMBER: 60/229,345

R APPLICATION NUMBER: 60/229,287

R APPLICATION NUMBER: 60/229,287

R PILING DATE: 2000-09-01

R APPLICATION NUMBER: 60/229,513

R APPLICATION NUMBER: 60/229,513

R APPLICATION NUMBER: 60/221,413

R APPLICATION NUMBER: 60/231,413
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R FILING DATE: 2000-08-14
R APPLICATION WIMBER: 60/225,213
R APPLICATION NUMBER: 60/225,213
RR APPLICATION NUMBER: 60/227,182
R FILING DATE: 2000-08-12
R FILING DATE: 2000-08-14
R FILING DATE: 2000-08-14
R FILING DATE: 2000-08-14
R FILING DATE: 2000-08-14
R FILING DATE: 2000-09-17
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APPLICATION NUMBER: 60/249,245
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,244
FILING DATE: 2000-11-17
                                                                                                                                                                            APPLICATION NUMBER: 60/229,509
FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/236,367
FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/237,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/226,681
FILING DATE: 2000-08-22
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FILING DATE: 2000-11-17
  PRIOR
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62 YKOTSVLENHHWRSAVGLIRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFR 121 SHIDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKY 338 219 YKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALLLATDISRQNEYLSLFR 122 SHLDRGDLCLEDTRHRHLVLQWALKCADICNPCRTWELSKQWSEKVTEEFFHQGDLERCK 159 VHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATL ö Length 211; Indels 48.1%; Score 1079; DB 10; llarity 98.1%; Pred. No. 4.7e-104; Conservative 1; Mismatches 3; HLGVSPLCDRHTESIANIQIGFMTYL 364 HIGUSPLCDRHTESIAXIQIGNYTYL 207 PRIOR FILING DATE: 2000-11-17
PRIOR PELICATION NUMBER: 60/249,264
PRIOR FILING DATE: 2000-11-17
PRIOR PELICATION NUMBER: 60/249,214
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20 APPLICATION DATE: 2000-10-20
APPLICATION NUMBER: 60/246,475 APPLICATION NUMBER: 60/231,243 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/233,065 FILING DATE: 2000-09-14 Query Match Best Local Similarity Matches 202; Conserv N 279 339 182 셤 ጽ 셤 8 d à à

RESULT 11 US-10-386-414-6 ; Sequence 6, Application US/10386414

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RESULT 13
US-10-627-929-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 IIPQAPLHLLDEDYLGQARHMLSKVGMMDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 FHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 FKLDWYTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259
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                                                                                             APPLICANT: Williamson, Mark W.
APPLICANT: Williamson, Mark W.
APPLICANT: Cook, William James
APPLICANT: Cook, William James
APPLICANT: Cook, William James
APPLICANT: MacBerh, Radiel E.
APPLICANT: MacBerh, Radiel E.
APPLICANT: Carroll, Joseph M.
APPLICANT: Carroll, Myoung
TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
FILE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
TITLE OF INVENTION: MYBER: US/10/386,414
CURRENT APPLICATION NUMBER: 09/426,282
PRIOR APPLICATION NUMBER: 09/426,265
PRIOR FILING DATE: 1999-10-25
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 09/330,970
PRIOR FILING DATE: 2000-01-28
PRIOR PELING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 09/860,193
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 09/80,193
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 09/80,30,83
PRIOR FILING DATE: 2001-03-10-31
PRIOR APPLICATION NUMBER: 09/33,082
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 09/833,082
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 09/833,082
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 19
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                  GENERAL INFORMATION:
APPLICANT: Roballer-Libermann, Rosana
APPLICANT: Robison, Keith E.
APPLICANT: White, David
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Publication No. US20030139578A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.
APPLICANT: COCKS, Benjamin G.
APPLICANT: COLEMAN, ROGET T.
US20040006016A1
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US-10-386-414-6
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US-10-272-970-17
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Best Local Simi
Matches 160;
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APPLICANT:
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APPLICANT: Fisher, Douglas A. TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING PDESA and PDESB FILE REFERENCE: PC-0054 CIP
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; OTHER INFORMATION: GenBank ID No. US20030139578A1 g1705952
US-10-272-970-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.7%; Score 555; DB 14; Length 6 Best Local Similarity 32.6%; Pred. No. 1.3e-48; Matches 127; Conservative 77; Mismatches 154; Indels
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Publication No. US20040018605A1
GENERAL INFORMATION:
APPLICANT: AU-Young, Janice; Cocks, Benjamin G.
APPLICANT: Coleman, Roger; Seilhamer, Jeffrey J.
APPLICANT: Fisher, Douglas A.
TITLE OF INVENTION: CYCLIC WICLEOTIDE PHOSPHODIESTERASES
FILE REFERENCE: PP-0057-4 CON
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                                                                                     CURRENT FILING DATE: 2002-10-15
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/454,060
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1996-03-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERL PROGRAM
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CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 99/454,060
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: US 08/974,565
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593 TASVEKSQVGFIDYIVHPLWETWA 616
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SOFWRARE: Patentin version 3.1
SEQ ID NO L
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Best Local Similarity
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US-10-442-675-2
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                                                                                                                                  ; OTHER INFORMATĪON: GenBank ID No. US20040018605A1 g1705952
US-10-627-929-9
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APPLICANT: RESINK, Annelies
APPLICANT: SCHWEIGHOFFER, Fabien
ITILE OF INVENTION: Molecular Target of Neurotoxicity
FILE REFERENCE: B0100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.6%; Score 551; DB 12; Best Local Similarity 31.8%; Pred. No. 4.3e-48; Matches 122; Conservative 84; Mismatches 152;
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CURRENT FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
LENGTH: 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EXONHIT THERAPEUTICS SA
PRIOR FILING DATE: 1997-11-19
            NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL Program
SEQ ID NO 9
                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: souris
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                                                         LENGTH: 610
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     117
                                    296 VKKLMHSSSLNNTSISRRGINTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 352
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                                                                                                                                        178 ANSVIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL
                                                                                                                                                                                                                                               413 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL
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                                                                                                         118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL
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Publication No. US20040086900A1
GENERAL INFORMATION
APPLICANT: Wigler, M.
APPLICANT: Wigler, M.
APPLICANT: Colicelli, J.
TITILE OF INTENTION WEACHOOK
CURRENT APPLICATION NUMBER: US/10/442,675
CURRENT FILING DATE: 2003-05-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.5%; Score 550; DB 16; Best Local Similarity 31.8%; Pred. No. 3.4e-48; Matches 122; Conservative 84; Mismatches 152;
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Fri May 28 08:14:00 2004

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Search completed: May 26, 2004, 09:42:42 Job time : 578 secs

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GenCore version 5.1.6
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using sw model protein search, 1 OM protein

May 26, 2004, 09:24:28 ; Search time 21 Seconds (without alignments) 1951.314 Million cell updates/sec Run on:

US-09-966-781A-1 2243 1 DQTALYIRMLGDVRVRSRAG.....DTDAAFELNSQLLPQENRLS Title: Perfect score: Sequence:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 78:*

1: Dir1:*

2: Dir2:*

3: Dir3:*

4: Dir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

3',5'-cyclic-AMP p 3',5'-cyclic-mucle 3',5'-cyclic-mucle phosphodiesterase cAMP phosphodieste 3',5'-cyclic-mucle cyclic-AMP phospho 3',5'cyclic-nucle
3',5'-cyclic-nucle
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hypothetical prote
hypothetical prote
3',5'-cyclic-nucle
3',5'-cyclic-nucle phosphodiesterase Description SUMMARIES A47286 UC7266 I53865 I53865 I53865 I53865 I615943 A40349 A40349 A60349 A60349 A6158 B53109 I67945 JMC089 A64162 A665548 JMC089 A665548 A76789 A7789 DB Query Match Length 100.0 Result . 8

cyclic nucleotide	cyclic nucleotide	3',5'-cyclic-nucle	cyclic-nucleotide	cGMP-inhibited cAM	3',5'-cyclic-GMP p	3',5'-cyclic-GMP p	3',5'-cyclic-nucle	3',5'-cyclic-nucle	3',5'-cyclic-GMP p	3',5'-cvclic-GMP p					
30901	370522	A40283	A48508	A44093	JW0106	A48719	A40981	JC2486	B34611	S30762	S13030	S06418	JC4520	A47451	A42828
H	O,														
2 T	7	N	N	N	Н	Н	Н	Н	7	0	7	Н	N	Н	0
2	1112 2 8	491 2	1108 2	1141 2	875 1	875 1	921 1	928 1	859 2	856 2	859 2	859 1	858 2	856 1	854
1054 2 T	_		17.2 1108 2	_											
1054 2 T	17.9	17.5	_	16.7	15.5	14.9	14.6	14.4	13.2	13.0	12.9	12.9	12.8	12.8	12.0

ALIGNMENTS

RESULT 1 A47286 2,5-cyclic-AMP pho C;Species: Homo sapi C;Date: 03-May-1994 C;Accession: A47286 R;Michaell, T.; Bloo. J. Biol. Chem. 269, J. Title: Isolation a A;Reference number: A;Accession: A47286 A;Accession: A47286 A;Catus: prelimina A;Molecule type: RR A;Residues: 1-498 a A;Cross-references: C;Superfamily: 3',5' C;Keywords: phosphon F;27-447/Domain: 3	RESULT 1 A47286 2.5-cryclic-AMP phosphodiesterase (EC 3.1.4) - human (fragment) C; 5-cryclic-AMP phosphodiesterase (EC 3.1.4) - human (fragment) C; 5-cryclic-AMP phosphodiesterase (EC 3.1.4) - human (fragment) C; 5-cryclic-AMP phosphone (man) C; 5-cryclic-AMP phosphone (man) C; 5-cryclic-AMP phosphone (man) C; 5-cryclic-AMP phosphone (man) C; 5-cryclic-AMP (m
Query Match Best Local Matches 42	ch 100.0%; Score 2243; DB 2; Length 498; 1 Similarity 100.0%; Pred. No. 6.2e-177; 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
S S	1 DQTALVIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
Qy Db	61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNPDIFLFDRLTNGNSLVSLTFF 120
% B	121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
Oy 1	181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
Qy 25	241 GLFSHLPLESROQMETQIGALILATDISRONEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
s da	301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
Oy 3	361 MTYLVEPLFTEWARFSNTRLSGTWLGHVGLNKASWKGLQREGSSSEDTDAAFELNSGLLP 420

421 QENRLS 426

à

3',5'-cyclic-nucle

PID

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A; Maccession: C32558
A; Molecule type: mRNA
C; Superfamily: a', 5' -cqlic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5', Meyology: cAMP binding; phosphoric diester hydrolase
F; 14-20/Region: responsible for membrane association
F; 14-20/Region: responsible for membrane association
F; 14-10/Region: x', 5' -cyclic-nucleotide phosphodiesterase 4A, splice form 3 #status
F; 18-10/Product: 3', 5' -cyclic-nucleotide phosphodiesterase 4A, splice form 2
F; 18-412/Domain: 3', 5' -cyclic-nucleotide phosphodiesterase homology CCNP>
                                                                                                                                                                             of the Drosophila dunce(+)
                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-598,'T',600-610 <DAV>
A;Cross-references: GB:M26715; NID:g203982; PIDN:AAC37699.1; PID:g203983; GB:J04554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: I53865
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
R;Bolger, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian A;Reference number: I53865; MUID:95047482; PMID:7958996
                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Rosidues: 85-120,154-598,'T',600-610 <DA2>
A;Cross-references: GB:M26716; GB:M26717; GB:U04554; NID:g203986; PIDN:AAA41102.1;
A;Note: splice form RD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 RWLGDVRVRSRAGFESERRGSHPYIDFRIFHSOSEIEVSVSARNIRRLLSFOR----YLR
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                                                                                        A; Cross-references: GB: L27062; NID: 9436013; PIDN: AAA56859.1; PID: 9436014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 24.7%; Score 555; DB 2; Length 61 Best Local Similarity 32.6%; Pred. No. 1.1e-37; Matches 127; Conservative 77; Mismatches 154; Indels
                                                                                                               Ribavis, R.L.; Takayasu, H.; Eberwine, M.; Myres, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 3604-3608, 1989
A;Title: Cloning and characterization of mammalian howologs
A;Reference number: A32558; MUID:89264472; PMID:2542942
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        from GB/EMBL/DDBJ
                                A; Molecule type: mRNA
A; Residues: 1-610 <RES>
           translated
                                                                                                                                                                                                                                  A; Accession: A32558
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NyAlternate names: cyclic AMP-specific phosphodiesterase RD1; RNPDE4A1
NyContains: 3',5'-cyclic-nucleotide phosphodiesterase AA, splice form 2 (cyclic AMP-spec
hosphodiesterase RD3)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Pay-1998 #sequence revision 29-May-1998 #text_change 24-Aug-2001
C;Accession: 167946; A32558; B32558; C32558
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 6q23-24
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: phosphoric diester hydrolase
                                                                                                                                 UCTION

3',5'-Cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human
3',5'-Cyclic-nucleotide phosphodiesterase 7B

C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C;Accession: JCT266
R;Sasaki, T.; Kotera, J.; Yuasa, K.; Omori, K.
Biochem. Biophys. Res. Commun. 271, 575-583, 2000
A;Title: Identification of human PDE7B, a cAMP-specific phosphodiesterase.
A;Reference number: JCT266
A;Aolecule type: mRNA
A;Residues: 1-450 <&ASA>
A;Cross-references: DDBJ:AB038040
A;Cross-references: DGBJ:AB038040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 62.6%; Score 1403.5; DB 2; Local Similarity 62.6%; Pred. No. 8.3e-108; Les 258; Conservative 66; Mismatches 87;
                             498
OENRLS
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 14-Jul.1994 #sequence_revision 14-Jul-1994 #text_change 21-Jul-2000
C;Date: 14-Jul.1994 #sequence_revision 14-Jul-1994 #text_change 21-Jul-2000
C;Date: 14-Jul.1994 #sequence_revision 14-Jul-1994 #text_change 21-Jul-2000
R;Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins, M.; Jarnagin, Gene 129, 239-247, 1993
A;Title: The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV) reveals a A;Title: The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV) reveals a A;Reference number: JC1519; MUID:93314968; PMID:8392015
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A;Cross-references: GB:L20971; NID:g347131; PIDN:AAA03593.1; PID:g347132
A;Cross-references: GB:L20971; NID:g347131; PIDN:AAA03593.1; PID:g347132
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5
C;Keywords: phosphoric diester hydrolase
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
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A;Experimental source: lymphocyte
A;Norce: only partial nucleotide sequence is given
R;McLaughlin, M.M.; Cieslinski, L.B.; Burman, M.; Torphy, T.J.; Livi, G.P.
J. Biol. Chem. 268, 6470-6476, 1993
A;Title: A low-Km, rolipram-sensitive, cAMP-specific phosphodiesterase from human braix
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A; Experimental source: frontal cortex
Mol. cell. Biol. 13, 6558-6571, 1993
A; Title: A family of human phosphodiesterases homologous to the dunce learning and memc A; Reference number: A54442; MUID:94019330; PMID:8413254
A; Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific (clone HBP106)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 NYTDRIQVLRNMYHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 433
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                                                                                                         254 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 313
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A, Accession: A45500
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llarity 31.8%; Pred. No. 2.5e-37;
Conservative 84; Mismatches 152;
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Best Local Similarity
Matches 122; Conserv
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A, Molecule type: mRNA
A, Residues: 1-564 < OBE>
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A; Residues: 1-564 <MCL>
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C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
F;231-459/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
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C;Species: Rattus norregicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 03-Nov-2000
C;Accession: 159143
R;Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wigler, M. Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989
A;Title: Isolation and characterization of a mammalian gene encoding a high-affinity A;Reference number: 159143; MUD:89264471; PMID:2542941
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C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology
F;418-646/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP:
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Best Local Similarity 32.6%; Pred. No. 1.7e-37;
Matches 127; Conservative 77; Mismatches 154;
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-844 <RES>
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Best Local Simi
Matches 122;
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A; Cross-references: GB:L20966; NID:g147121; PIDN:AAA03589.1; PID:g347122
C; Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',!
F;405-633/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
C;Accession: 161354
R;Bolger, G; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, Mol. Cell. Biol. 13, 6558-6571, 1993
A;Pitle: A family of human phosphodiesterases homologous to the dunce learning and memc A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 DTRHRHIVLOMALKCADICNPCRTWELSKOWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 DAVFTDLEILAAIFPAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL
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   QRYLRSSRFFRGTAVSN-SLN1LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL
                                      118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL
                                                                                                                                                                                                                                                                                     ----RGDLCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR-----LLLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL
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                                                                                                                                                              178 ANSVIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL
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Best Local Similarity 31.8%
Matches 122; Conservative
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Ayithe: Modecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989

Ayithe: Modecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP proc. Natl. Acession: D33904

Ayacession: D33904

Ayacession: D33904

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Ayacession: D33904

Ayacession: D33904

Ayacession: Asidos MulD: Bylosion

Bymonaco, L.; Vicini, R.; Coni, M.

Bymonaco, L.; Vicini, R.; Coni, M.

Bymonaco, L.; Vicini, R.; Coni, M.

Ayacession: Asidos MulD: 94103234; PMID: 8276818

Ayacession: Asidos MulD: 94103234; PMID: 8276818

Ayacession: Asidos MulD: 94103234; PMID: 8276818

Ayacession: Asidos MulD: 94103234; PMID: 9409828

Ayacession: Asidos MulD: 9409826; FIDN: AAA18926.1; FID: 9409828

Ayacession: Isia Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

Ayacession: Isia Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

Ayacession: Isia Rodgers, L.K.; Riggs, M.

Ayacession: Isia Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

Ayacession: Isia Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

Ayacession: Isia Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

Ayacession: Isia Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

Ayacession: Isia Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

Ayacession: Isia Rodgers, L.K.; Riggs, M.

Ayacession: Isia Rodgers, 
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A40949

Yordic-AMP phosphodiesterase (EC 3.1.4.-) - rat
NyAlternate names: PDS4/IVb long form
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-May-1992 #sequence revision 13-May-1992 #text_change 09-Jun-2000
C;Accession: A40949; D33904; Ā53109; 167942
R;Swinnen, U.V.; Tsikalas, K.E.; Contt, M.
J. Biol. Chem. 266, 18370-18377, 1991
M. Ficher Properties and hormonal regulation of two structurally related cAMP phosphodies A;Reference number: A40949; MUID:92011578; PMID:1655746
A;Retus: preliminary
A;Molecule type: mRNA
A;Residues: 1-564 <SWI>A;Crose-references: GBMX5350
B;Crose-references: GBMX5350
B;Crose-references: GBMX5350
B;Crose-references: GBMX5350
B;Crose-references: GBMX5350
B;Crose-references: GBMX5350
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A;Residues: 1-564 <RES>
A;Cross-references: GB:1.27058; NID:g950096; PIDN:AAA74478.1; PID:g598375
C;Superfamily: 3',5'-cyclic-nuclectide phosphodiesterase 1B, calmodulin-dependent; 3',5'C;Reywords: alternative initiators; alternative splicing; phosphoric diester hydrolase F;233-461/Domain: 3',5'-cyclic-nuclectide phosphodiesterase homology <CNP>
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                                                                                          315
                                                                                                                                                                                    316 QEEHCDIFMALTXKORQTLRKAVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD
                                ANSVTPWDILLISLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL
                                                             DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL
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ilarity 31.8%; Pred. No. 2.5e-37;
Conservative 84; Mismatches 152:
                                                                                                                                                                                                                                                                                                                                                                                                                                   350 TESIANIQIGEMIYLVEPLFTEWA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Best Local 9
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C;Date: 26-Jul-1996 #Bequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: A54442; S55788; A36317; S55787
C;Accession: A54442; S55788; A36317; S55787
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memc A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: A54442
A;Accession: A54442
A;Accession: A54442
A;Reiduus: translated from GB/EMBL/DDBJ
A;Reiduus: translated from GB/EMBL/DDBJ
A;Reiduus: 1-886 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 'MCPFPVTTV',210-735,'E',737-886 <SUL>
A; Residues: 'MCPFPVTTV',210-735,'E',737-886 <SUL>
A; Cross-references: EMBL:138087; NID:9604374; PIDN:AAC50458.1; PID:9604375
A; Note: 736-Ala was also found
R; Livi, G.P.; Kmetz, P.; McHale, M.M.; Cieslinski, L.B.; Sathe, G.M.; Taylor, D.P.; Dav
Mol. Cell. Biol. 10, 2678-2686, 1990
A; Title: Cloning and expression of cDNA for a human low-K-m, rolipram-sensitive cyclic
A; Reference number: A36317; MUID:90258854; PMID:2160582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'MCPPPUTU',210-516,'Y',518-722,'R',724-726,'R',728-735,'E',737-788,'E',79(
A;Cross-references: GB:M37744
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
B53109
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4B, cAMP-specific, splice form
                                                                                                                                                                                                                                                                                      A,Cross-references: GB:L20965; NID:g347119; PIDN:AAA03588.1; PID:g347120
R;Sullivan, M.; Egerton, M.; Shakur, Y.; Marquardsen, A.; Houslay, M.D.
Cell. Signal. 6, 793-812, 1994
A;Title: Molecular cloning and expression, in both COS-1 cells and S. cerevisiae, A;Reference number: S55788; MUID:95194817; PMID:7888306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 19p13.1-19q12
C,Superfamily: 3',5'-cyclic-incleotide phosphodiesterase homology
C,Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F,432-660/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMSRSGNQVSEXISTTFLDKQNEVEIPSPTMKEREKQQAPRPRPSQPPPPVPHLQPMSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 DAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515 QEDNCDIFONLSKRORÓSLRKMVIDMVLÁTDMSKHMTLLADLKTMVETKKVTSSGVLLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 ITGLKKLMHSNSLNNSNIPRFGVKTDQEELLAQELENLNKWGLNIFCVSDYAGGRSLTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 RESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD-----RGDLCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 ESERRGSH--PYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.1%; Score 541; DB 2; 32.3%; Pred. No. 2.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 TESIANIQIGEMTYLVEPLETEWA 373
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TASVEKSQVGFIDYIVHPLWETWA
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Gene 138, 253-256, 1994
A;Title: Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP phosphodiest
A;Reference number: I38416; MUID:94171048; PMID:8125310
                                                                                                                                        3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific - human N'Alternate names: 3',5'-cyclic-AMP phosphodiesterase, rolipram-sensitive C;Species: Home sapiens man)
C;Decise: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
C;Accession: 161358; 138416
E;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memor A;Reference number: A54442; MUID:94019330; PMID:8413254
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A54442
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, cAMP-specific, long splice N;Contains: 3',5'-cyclic AMP phosphodiesterase HPDE4A6 splice form C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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LLQEENCDIFQNLTKKQRQSLRKGVVIDIVLATDMSKHMNLLADLKTMVETKKVTSSGVLL 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 70-507, P',509-673 <RE2>
A;Cross-references: EMBL:U02882; NID:g433346; PIDN:AAC13745.1; PID:g433347
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A;Molecule type: mRNA
A;Residues: 1-673 <RES>
A;Cross-references: GB:L20970; NID:g347129; PIDN:AAA03592.1; PID:g347130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodul
C;Keywords: cAMP binding; phosphoric diester hydrolase
F;325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 542; DB 2; Length 673; Pred. No. 1.5e-36; 82; Mismatches 150; Indels
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A, Map position: 5q12-5q12
      631
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                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: 161358
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A,Gene: PDE3/IVd gene
C,Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',!
C,Keywords: CAMP binding; phosphoric diester hydrolase
F;325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: A53678
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Fesidues: 167-672 - KRB2>
A,Cross-references: EMBL:U09456; NID:g517416; PIDN:AAA20393.1; PID:g517417
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian general a,Reference number: 153865; MUID:95047482; PMID:7958996
A,Accession: 167943
                                                                                                                                                                                                                                                                                                                                                                                                                  gene codes for multiple proteins differentia PMID:8034568
                                                                                                                                  3.,5. cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific, splice form N.Alternate names: cyclic-AMP phosphodiesterase
N.Alternate names: cyclic-AMP phosphodiesterase
N.Contains: 3.,5. cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific, C.5 Species: Rattus norvegicus (Norway rat)
C.5Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 17-Nov-2000
C.Accession: I61259; A53678; I67943
R.Sette, C.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 18271-18274, 1994
A.Title: The rarePBE3/Ivd phosphodiesterase gene codes for multiple proteins differenti. A.Reference number: A53678; MUID:94308045; PMID:8034568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 KIMHSS-----SLINSCIPRFGYKIBOBDVLAK-BLEDVNKWGLHVFRIAELSGNRPLT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 VIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAADVVQSTHVLLSTP 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 ALEAVFIDLEILAAIFASAIHDVDHPGVSNQFLININSELALMYNDSSVLENHHLAVGFK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYLRSSRFFRGTAVSNS----LNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 KLANSVTFWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 LLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD-----RGDLC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 RELTHLSEMSRSGNQVSEYISNTFLD-----KÖHËVEIPSPTQKEKEKKKRPMSQISGVK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 LEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCD 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 'N',96-625,'Y',627-672 <RE3>
A;Cross-references: GB:L27059; NID:g436007; PIDN:AAA56857.1; PID:g436008
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 672;
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A;Molecule type: mRNA
A;Residues: 1-672 <RRS>
A;Cross-references: EMBL:U09457; NID:g517418; PID:g517419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
24.0%; Score 539; DB 2; L.
Best Local Similarity 31.6%; Pred. No. 2.6e-36;
Matches 122; Conservative 81; Mismatches 151;
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A.Residues: YEPGES: /34-421,/E',423-584 <RES>
A.Cross-references: GB:L27060; NID:g436009; PID:g436010
C.Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Reywords: alternative initiators; alternative splicing; cAMP binding; phosphoric diest
F;237-465/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:U01280
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 8197-8201, 1989
A;Title: The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hormon A;Reference number: A34414; MUID:90046763; PMID:2554303
A;Accession: A34414
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Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A; Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP A; Reference number: A33904; MUID:89315790; PMID:2546153
A; Status: preliminary
                                                                                                                                                                         related rolipram-sensitive cAMP
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text_change 19-May-2000
C;Date: 07-Jul-1999; A34414; C33904; 167944
R;Monaco, L.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 347-357, 1994
A;Fitle: Structure of two rat genes coding for closely related rolipram-sens A;Reference number: A53109; MUID:94103234; PMID:8276818
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A, Residues: 144-480 CSW2>
A, Residues: 144-480 CSW2>
A, Cross-references: GB:W25349
R; Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A; Title: Differential CNS expression of alternative mRNA isoforms of
A; Reference number: 153865; MUID:95047482; PMID:7958996
A; Actual: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: MRNA
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A; Residues: 1-584 <SWI>
                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA A; Residues: 1-584 < MON >
                                                                                                                                                                                                                                     A; Accession: B53109
A; Status: preliminary
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calmodulin-dependent; 3', E

Length 536; Indels

DB 2;

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A; Molecule type: mRNA
A; Residues: 1-536 <RES>
A; Cross-references: GB:L27061; NID:g436011; PIDN:AAA56858.1; PID:g436012
B; Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A; Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce CAMP
A; Reference number: A33904; MUID:89315790; PMID:2546153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 ADTLLRYLLTLEGHYHSNVAYHNSIHAADVVQSAHVLLGTPALEAVFTDLEVLAAIFACA 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 PRFGVQTDQEEQLAK-ELEDTNKWGLDVFKVAELSGNRPLTAVIFRVLQERDLLKTFQIP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QMETQIGALILATDISRQNEYLSLFRSHLDR-----GDLCLEDTRHRHLVLQMALKCAD 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 ETSRSGNQVSEYISQTFLDQQAEVELPAPPTEDHPWPMAQITGLRKSCHTS---LPTAAI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Residues: 230-496 <SWI>
A, Cross-references: GB: MZ347, GB: WZ8410
C; Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-deper C; Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase to diester hydrolase F; 253-481/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
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C;Accession: I67945; A33904
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.8%; Score 534.5; DB 2; 32.2%; Pred. No. 4.5e-36; tive 71; Mismatches 159;
                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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es 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A33904
A; Status: preliminary
A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMED: 246632; NID: 9727222; PIDN: CAA86601.1; PID: 9727223
A; Experimental source: substantia nigra
R; Bolger, G; Mccheall, T; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
M; Bolger, G; Mccheall, T; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
M; Title: A family of human phosphodiesterases homologous to the dunce learning and memor
A; Reference number: A5442; MUID: 94019330; PMID: 8413254
A; Recession: 161356
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Retais preliminary; translated from GB/EMBL/DDBJ
A; Residues: 462-712 <RES>
A; Cross-references: GB: L20968; NID: 9347125; PIDN: AAA03591.1; PID: 9347126
C; Genetics:
A; Description: CAMP hydrolysis; converts CAMP to non-cyclic AMP
A; Pathway: cyclic nucleotide metabolism
A; Description: CAMP hydrolysis; converts CAMP to non-cyclic AMP
A; Rathway: cyclic nucleotide metabolism
A; Description: CAMP hydrolysis; converts CAMP to non-cyclic AMP
C; Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3', 5'
C; Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>
C; Keywords: phosphoric diester hydrolase
F; 387-615/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>
                               3',5'-cyclic-nucleotide phosphodiesterase (BC 3.1.4.17), cAMP-specific - human N;Alternate names: 3',5'-cyclic AMP phosphodiesterase S,5'-cyclic AMP phosphodiesterase S,5'-cyclic AMP phosphodiesterase C;Specias: Homo sapiens (man) C;Date: 27-Mov-1997 #sequence_revision 12-Dec-1997 #text_change 17-Nov-2000 C;Accession: S71626; I61356 C;Accession: S71626; I61356 Mueller, T.; Luebbert, H. FEBS Lett. 358, 305-310, 1995 A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific; A;Reference number: S71626; MUID:95145731; PMID:7843419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 I-----LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESG--LFSHLPLE 249
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33.2%; Pred. No. 5e-36;
tive 70; Mismatches 153; Indels
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-712 < ENG>
                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                               A;Accession: S71626
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C;Date: 18-Jun-1998 #sequence_revision 26-Aug-1999 #text_change 21-Jul-2000 C;Accession: JW0088 #sequence_revision 26-Aug-1999 #text_change 21-Jul-2000 C;Accession: JW0088 Bsequence_revision J.S.; St Denis, S.H.; Cheng, J.B. Biochem: Date, Res. Commun. 246, 570-577, 1998 AjTitle: Isolation and characterization of PDERA, a novel human cAMP-specific phosphod: A;Reference number: JW0088; MUID:98289571; PMID:9618252 A;Accession: JW0088.
3',5'-cyclic-nuclectide phosphodiesterase (EC 3.1.4.17) 8A, high affinity cAMP-specific N/Alternate names: high affinity cAMP-specific phosphodiesterase PDE8A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-713 <FIS-
A;Cross-references: GB:AF056490; NID:g3184388; PIDN:AAC39763.1; PID:g3184389
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 8A, high affinity cAMP-specif:
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
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167945
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - rat (fragment)
N;Alternate names: cAMP phosphodiesterase 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Nov-2000

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54 RLLSFQRYLRSSRFFRGTAVSNSLNILD----DDYNGQAKCMLEKVGNWNFDIFLFDRLT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYFGQNPYHNAVHAADVTQAMH 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 HNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIEANYHSSNPYHNSTHSADVLHATA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454 YFLSKERIKETLDPIDEVAALIAATHHOVDHPGRTNSFLCNAGSELAILYNDTAVLESHH 513
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F;439-680/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               32;
                                                                                                                         Query Match 22.4%; Score 503; DB 2; Length 713; Best Local Similarity 31.6%; Pred. No. 2.6e-33; Matches 117; Conservative 76; Mismatches 145; Indels
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Search completed: May 26, 2004, 09:25:36 Job time: 22 secs

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RESULT
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28iv84 homo sapien
343850 homo sapien
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                                                                                                                                                                                                       May 26, 2004, 09:24:28; Search time 46 Seconds (without alignments) 2921.973 Million cell updates/sec
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1 DQTALYIRMLGDVRVRSRAG.....DTDAAFELNSQLLPQENRLS
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     OM protein - protein search, using sw model
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Q8TE4
Q9BZ40
Q8CBS2
Q8VIE2
Q8VIE3
Q9EQK7
Q9EQK7
Q9QXI7
Q91VY2
Q91VY2
Q11345
Q11345
Q8VB12
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Q8VB13
Q8VB2
Q8V
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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ALIGNMENTS

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XECOLOT I	710	Q96T72;	DT 01-DEC-2001 (TrEMBLrel. 19, Created) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	01-OCT-2003 (7	cAMP-specific cyclic nucleot	Homo sapiens (Human).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	NCBI TaxID=9606:	RN [1]		MEDLINE=21265467; PubMed=11371644;	5				AAK57640.1;	GO; GO: VOUGHIL4; FIST, ST -CYCLIC-INCLEOCIDE PROSPROGIESTERASE A;	3 6	InterPro; IPR003607; Met phsphohydro.				-	PROSITIE; PS00126; PDEASE I; 1.	SQ SEQUENCE 424 AA; 48827 MW; A7DBF40D08A7B561 CRC64;	85.2%;	Best Local Similarity 99.5%; Pred. No. 8.4e-164; Matches 362; Conservative 0; Mismatches 2; Indels 0; Gaps	QY 1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR	And the second of the second o	ñ
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amoutation update)
BA472E5.1 (High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase
(EC 3.1.4.17, rolipram-insensitive phosphodiesterase type 7))
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                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AL138828; CAC27545.1;
GO, GO:0004114; F:33, 55-cyclic-nucleotide phosphodiesterase GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR003607; Met Phephohydro.
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Best Local Similarity 62.8%; Pred. No. 1e-115;
Matches 252; Conservative 65; Mismatches 83; Indels
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PRINTS; PR00387; PDIESTERASE1.
SWART; SM00471; HDc; 1.
PROSITE; PS00126; PDEASE_1; 1.
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SEQUENCE FROM N.A.
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SEQUENCE
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Q9BZ40;
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                                                                                                                       LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
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YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
                                                     YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 176
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                                                                                                                                                         1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR
                                                                                                                                                                                                                                        VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki T., Kotera J., Omori K.;
"Novel alternative splice variants of rat PDE7B.";
"Novel alternative splice variants of rat PDE7B.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB054409; BAD75637.1;
GO, GO:000114; F.3', 5'-cyclic-nucleotide phosphodiesterase a.
GO, GO:0001678; F.hydrolase activity; IEA.
InterPro; IPR003607; Met_phsphohydro.
InterPro; IPR002073; PDEase.
Pfam; PF002033; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.9%; Score 1389.5; DB 11; Length 446; 62.4%; Pred. No. 8.9e-117; ive 65; Mismatches 85; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ol-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Cyclic nucleotide phosphodiesterase 7B1 (EC 3.1.4.17). RNPDE7B.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity
Matches 257; Conserv
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01-MAR-2002 (
01-JUN-2003 (
                                                                                                                              Q8VIE2;
01-MAR-2002
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ID QB1
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Q8VIE2
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YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).

BMBL, AK035385; BAC25052.1; -.

MGD; MGI:1352752; Pde7b.

GO; GO:0004115; F:CAMP-specific phosphodiesterase activity; IDA.

FILEFPC: IPR003607; Met phsphohydro.

FILEFPC: IPR00307; PDEase.

Pfam; PF00233; PDEase: 1.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                             411
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SMART; SW00471; HDC; 1.
PROSITE; PS00126; PDEASE 1; 1.
SEQUENCE 446 AA, 51307 MW; 7C002364B396A5A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                             WARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA
                                                                                                                              361 WAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS
                                                                                                                                                                                                                                                                                                                   446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUB=Urinary bladder;
MEDLINE=22354683; PubMed=12466851;
The FANTOM COnsortium,
                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLES 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 ROOMETOIGALILATDISRONEYLSLFRSHLDRGDLCLEDTRHRHLVLOMALKCADICNP 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 GDVRLRGQTGVPAERRGSYPFIDFRLINNTTHSGEIGSKKKVRRLLSFQRHFHESRLLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 FHIDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLENIQDRHFMLQIALKCADICNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 GDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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"Novel alternative splice variants of rat PDE7B.";
"Novel alternative splice variants of rat PDE7B.";
submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB057411; BAB75639.1; -.
GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a.
GO; GO:0015787; F:hydrolase activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR003607; Met_phsphohydro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.4%; Score 1377.5; DB 11; Lengt
63.2%; Pred. No. 1.1e-115;
iive 63; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 EWARFS-NTRLSQTMLGHVGLNKASWKGL----QREQSSSED 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           459 AA; 52680 MW; A3F26E95C7FC00A5 CRC64;
                                                  01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-UUN-2003 (TrEMBLrel. 24, Last annotation update) Cyclic nucleotide phosphodiesterase 784 (EC 3.1.4.17)
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
   Ä
   459
   PRT;
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PRINTS; PRO0437; PDIESTERASE1.
SMART; SMO471; HDC; 1.
PROSITE; PS00126; PDEASE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254; Conservative
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PRELIMINARY;
                                                                                                                                                                                                              Rattus norvegicus (Rat).
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., IEA.

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SSR-----FFRGTAVSNSLNI-----LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 25, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Cyclic AMP phosphodesterase PDE4A10 (Fragment).
Rattus norvegiaus (Rat).
Rattus norvegiaus (Rat).
Mammalia; Butheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 DQTALYIRMLGDVKVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rena G., Begg F., Ross A., MacKenzie C., McPhee I., Campbell L.,
Huston B., Sullivan M., Houslay M.D.;
Molecular cloning, genomic positioning, promoter identification
characterisation of the novel cAMP-specific phosphodiesterase,
PDE4ALO.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Pharmacol. 0:0-0(2001).

Mol. Pharmacol. 0:0-0(2001).

Mol. April451-22.

GO; GO:0004114; F:3', 5'-cyclic-nucleotide phosphodiesterase a. .

GO; GO:0004114; F:3', 5'-cyclic activity; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR005607; PDEase.

InterPro; IPR002073; PDEase.
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                                                                                Zhou L., Thompson W.J., Potter D.B.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, A2266344, AAP31235.1, -..
GO; GO:0004114; F:3', 5'-cyclic-nucleotide phosphodiesterase a.
GO; GO:0007165; P:signal transduction; IEA.
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                                                                                                                                                                                                                                                                                                      162 162
162 AA; 18867 MW; E7D548571291EEDA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0 3
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.0%; Score 717; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.1e-56;
Matches 139; Conservative 0; Mismatches 0;
invest. Ophthalmol. Vis. Sci. 40:1745-1752(1999)
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PRINTS; PR00387; PDIESTERASE1.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 SKQWSERVCEEFYRQGDLEQKFELEISPLCNQQKDSIPSIQIGFWTYIVEPLFREWARFT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 LNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYFHLDMM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 KLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 TLHRFLVMVQEDYHGHNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMET 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWEL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .; IEA.
                                                                       Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Rattus.
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MEDLINE=99320215; PubMed=10393044;
MEDLINE=99320215; PubMed=10393044;
Zhou Li, Thompson W.J., Potter D.E.;
"Multiple cyclic nucleotide phosphodiesterases in human trabecular meshwork cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                  TISSUB-Testis;
Sasaki T., Kotera J., Omori K.;
Sasaki T., Kotera J., Omori K.;
Sasaki T., Kotera J., Omori K.;
"Novel alternative splice variants of rat PDE7B.";
"Novel alternative splice variants of rat PDE7B.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB057410; BA87-5011, Cote EMBL/GenBank/DDBJ databases.
GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a.
GO; GO:00165; P:signal transduction; IRA.
InterPro; IPR003607; Met_phsphohydro.
InterPro; IPR002073; P)Ease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length 359;
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67.0%; Pred. No. 1.2e-102;
tive 51; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 AA; 41456 MW; OFF72792737CE48A CRC64;
            Cyclic nucleotide phosphodiesterase 7B3 (EC 3.1.4.17)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 -NTRLSQTMLGHVGLNKASWKGL----OREOSSSED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00126; PDEASE I; 1.
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PRINTS; PR00387; PDIESTERASE1
SMART; SM00471; HDc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 225; Conserva
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257
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QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : | | : | | : : | : : | : : | SELTHISEMSRSGNQVSEYISNTELD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 VKKIMHSSSINNTSISRFGVNTENEDHLAKE---LEDLINKWGLNIFNVAGYSHNRPLICI 173
                                                                                                                                                                                                                                                                                                                                                                                                               : | ||: : |||: ||: || ||: || 333 NYTORIQVIRNAVHCADLSNPTKSLELYRQWTDRIMEBFFQQGDKERERGMEISFWCDKH
                  QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL
                                                                     296 VKKLMHSSSLANTSISRFGINTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI
                                                                                                                                   118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL
                                                                                                                                                                            178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL
                                                                                                                                                                                                                                                                                                                                                                               RES--GLESHLPLESROOMETQIGALILATDISRONEYLSLFRSHLD-----RGDLCLE
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OEC-2003 (TrEMBLrel. 25, Last annotation update)
similar to phosphodiesterase 4B, CAMP-specific (Dunce (Drosophila))
homolog phosphodiesterase E4) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MRR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC007155; AAH07155.1; -.

EMBL; BC007155; AAH07155.1; -.

MGD; MGI:105923; Edhra.

MGD; MGI:9957; Pedabra.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.5%; Score 550; DB 11;
31.8%; Pred. No. 7.2e-41;
iive 84; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Breast tumor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
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242 QSQPMSQITGLKKLVHTGSLNTNVPRFGVKTDQEDLLAQELENLSKWGLNIFCVSEYAGG 301
                                                                                    112 NSLVSLIFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171
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                                                                                                                                                                                                                                              ||:| :| :| :| :| :| :| VGFKLLQEENCDIFQNLSKRQRQSLRKAVIDMVLATDMSKHMTLLADLKTMVBTKKVTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                       LKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWR
                                                                                                                                                                                                                                                                                                                                232 SAVGLIRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD-----R
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Cherry J.A., Thompson B.E., Pho V.;
Cherry J.A., Thompson B.E., Pho V.;
Thompson J.E., Thompson B.E., Pho V.;
Thompson and rollpram differentially inhibit cAMP-specific
phosphodiesterases PDB441 and PDB4B3 in the mouse.";
D. Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
REBL; AF208032; AFF19202.2;
REBL; AF208033; AFF19202.2;
REBL; AJ297397; CAB96770.1;
REBL; AJ297397; CAB96770.1;
REBL; AG09004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. ..;
RO; GO:0007165; P:signal transduction; IEA.
RICHERPEO; IPR003607; Met phephohydro.
RILHERPEO; IPR002037; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSOSEIEVSVSARNIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=SWISS WEBSTER, Cherry J.A., Thompson B.E., Pho V.; "Cloning and biochemical characterization of cyclic AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphodiesterase isoforms in the mouse.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
cAMP-specific phosphodiesterase (Phosphodiesterase 4B, specific).
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Prim; Pr0023; PDESSe; 1.
PRINTS; PR0039; PDIESTERASE1.
SMART; SM00471; HDc; 1.
PROSITE; PS00126; PDEASE I; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (Mouse).
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Matches 122; Conserv
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SEQUENCE FROM
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Q9QXI7
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118 TEHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
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                                                                                                                      59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSOSEIEVSVSARNIRR------LLLSF
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                                                                                                  290 DIRHRHLVLQMALKCADICNPCRIWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH
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                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                     358 QEEHCDIFMAUTKKQRQTLRKAWIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD
298 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL
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EMBL, AF202733, AAL31764.1; ---

GO, GO:0004114; F:3', 5'-cyclic-nucleotide phosphodiesterase a.

GO, GO:0009824; F:catalytic activity; IEA.

GO, GO:0007165; P:signal transduction; IEA.

InterPro; IPR003607; Met phsphohydro.

InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 24.5%; Score 550; DB 11; Length 659; Local Similarity 31.8%; Pred. No. 9.5e-41; les 122; Conservative 84; Mismatches 152; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olsen A.E., Bolger G.B.;
"Novel PDE4B cAMP-specific phosphodiesterase isoforms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00387; PDIESTERASE1.
SMART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE I; 1.
SEQUENCE 659 AA; 75059 MW; 500099DIE38E0882 CRC64;
                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (T-EMBLrel. 20, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) cAMP-specific phosphodiesterase isoform PDE484.
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STRAIN-Sprague-Dawley; TISSUE-Brain cortex;
                                                                                                                                                                                                                                                                                               629
                                                                                                                                                                        350 TESIANIQIGEMTYLVEPLETEWA 373
                                                                                                                                                                                            478 TASVEKSQVGFIDYIVHPLWETWA 501
                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Matches
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Q8VD81
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                                                                                                                           289
                                                                                                                                                                                              290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
                                                                                                                                                                                                                  354 NYTDRIQVLRNMVHCADLSNPTKSLBLYRQWTDRIMBEFPQQGDKERERGMEISPWCDKH 413
   174 MYAIFQERDLIKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 233
                                                         237
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MEDLINE=93314968; PubMed=8392015;
Obernolte R., Bhakta S., Alvarez R., Bach C., Mulkins M., Jarnagin K.,
Shelton E.R.;
                                                                           234 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL
                                                                                                                                                 RES--GLFSHLPLESROOMETQIGALILATDISRONEYLSLFRSHLD------RGDLCLE
                                                       178 ANSVIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The CDNA of a human lymphocyte cyclic-AMP phosphodiesterase (Pr reveals a multigene family.";
Gene 129:239-247(1993).
EMBL; 112686; AAA35643.1; -.
EMBL; 1012689; JC1519;
GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a...
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR003607; Met phephohydro.
InterPro; IPR002073; PDEase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.5%; Score 550; DB 4; 31.8%; Pred. No. 8.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                        606 AA.
                                                                                                                                                                                                                                                                                      | |: |: |: || |: || || TASVEKSQVGFIDYIVHPLWETWA 437
                                                                                                                                                                                                                                                                    TESIANIQIGEMIYLVEPLFTEWA 373
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PRINTS; PR00387; PDIESTERASE1
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Best Local Similarity 31.8*
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Human)
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SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 MYAIFQERDLIKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RES--GLESHLPLESROOMETQIGALILATDISRONEYISLFRSHLD------RGDLCLE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 ORYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
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NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                          N [1]

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=DBA/2J, and CS7BL/6J; TISSUE=Brain;

A Fehr C., Belknap J.K., Crabbe J.C., Buck K.J.;

T ethanol witchdrawal on mouse chromosome 4 and characterization of potential candidate genes.

T submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF326555, AAL37402.1;

EMBL; AF326555, AAL37401.1;

GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a...; I: GO; GO:0001165; P:signal transduction; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR003607; Met_phsphohydro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.5%; Score 550; DB 11; Length 7. 31.8%; Pred. No. 1.1e-40; ive 84; Mismatches 152; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
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SEQUENCE 721 AA; 82075 MW; B3725A478A7612FB
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                                                373
                                                                         Created)
                                                                                                                                                                                                       PRT;
                                                TESIANIQIGEMTYLVEPLETEWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00387; PDIESTERASEL SMART; SM00471; HDc; 1.
                                                                                                                                                                                                                                              (TrEMBLrel. 20, (TrEMBLrel. 20, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 31.8
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00233; PDEase; 1
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLre
Phosphodiesterase 4B.
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                   01-MAR-2002
                                                                                                                                                                                                                                                                       01-MAR-2002
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                                                                                                                                                           RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 TEHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 ANSVIPWDILLISLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 RES--GLFSHLPLESRQQMETQIGALILATDISRONEYLSLFRSHLD------RGDLCLE
                                                                                                                                                                                               Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                          related
                                                                                                                                                                                                                                                                                                                                                                                                 technology.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF202732; AAL31763.1;
GO; GO:000414; F:3.5/-GYClic-nucleotide phosphodiesterase a.
GO; GO:0003824; F:Gatalytic activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR003607; Met phsphohydro.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 736;
                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
Olsen A.E., Bolger G.B.;
"Novel PDE4B cAMP-specific phosphodiesterase isoforms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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PRINTS; PR00387; PDIESTERASE1.
SMART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE I; 1.
SEQUENCE 736 AA; 83348 WW; E78509269A8DF169 CRC64;
                                       01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
cAMP-specific phosphodiesterase isoform PDE4B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBIV84;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.5%; Score 550; DB 11; Best Local Similarity 31.8%; Pred. No. 1.1e-40; Matches 122; Conservative 84; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥.
736 AA.
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                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                             Rattus norvegicus (Rat).
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 KLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 KLMHSS-----SLTNSSIPRFGVKTEQEDVLAK-ELEDVNKWGLHVFRIAELSGNRPLT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 SLIFHLESLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVIQAMHCYLKEP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 ALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSSVLENHHLAVGFK 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIRES--GLFSHLPLESROOMETQIGALILATDISRONEYLSLFRSHLD------RGDLC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEDIRHRHLVLQMALKCADICNPCRIWELSKQWSEKVTERFFHQGDIEKKYHLGVSPLCD 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 RYLRSSRFFRGTAVSNS----LNILDDDYNGOAKCMLEKVGNWNFDIFLFDRLTNGNSLV 115
                                                                                                                                                                                                                                                                                                                                                                                                                        ----SVSARNIRRLLSFQ 59
                                                                                                                                                                                                             . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
                                                                                                                                                      Wang D. Bugaj-Gaveda B., Kwan M., Unterbeck A., De Vivo M.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AR536977; AAN10119-1; -.

GO, GO.00041118-1; F:3',5'-cyclic-nucleotide phosphodiesterase a.

GO, GO.00071465; P:3ignal transduction; IEA.

InterPro; IPR002073; PDEase.

Pfam; PF00233; PDEASE. 1.

PRINTS; PR001387; PDIESTERASE1.

PROSITE; PS00126; PDEASE I; 1.

SEQUENCE 687 AA, 77646 MW; 91137D110DC3477C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                     Query Match 24.4%; Score 548; DB 4; Length 687; Best Local Similarity 31.9%; Pred. No. 1.5e-40; Matches 123; Conservative 82; Mismatches 149; Indels
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
CAMP-specific phosphodiesterase PDE4D8.
                                                                                                                                                                                                                                                                                                                                                                                                                            8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEV--
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SEQUENCE FROM N.A.
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Search completed: May 26, 2004, 09:26:36 Job time : 48 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model using protein search, OM protein May 26, 2004, 09:24:28; Search time 97 Seconds (without alignments) 1240.879 Million cell updates/sec Run on:

Title: Perfect

1 DQTALYIRMLGDVRVRSRAG.......DTDAAFELNSQLLPQENRLS 426 US-09-966-781A-1 2243 score:

Sequence:

1586107 segs, 282547505 residues , Gapext 0.5 BLOSUM62 Gapop 10.0 Scoring table: Searched:

1586107

seq length: 0 seq length: 200000000 Minimum DB : Maximum DB :

Total number of hits satisfying chosen parameters:

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*			SUMMAKIES	
ns N	Score	ch	Length	DB	ΙD	Description
 	2243	100.0	426	5	AAE24527	Aae24527 Human PDE
2	2243	100.0	446	Ŋ	AAE24532	Human
m	2243	100.0	482	2	AAE24531	Aae24531 Human PDE
4	2243	100.0	498	~	AAW00094	Aaw00094 cAMP phos
2	2243	100.0	498	7	AAY49808	
9	2243	100.0	49	ᡢ	AAB20619	pTM2
7	2116	94.3		Ŋ	AAE24529	Aae24529 Rat PDE7
00	2116	94.3		Ŋ	AAE24533	Rat PD
o.	2105	93.8		2	AAE24528	Aae24528 Mouse PDE
10	2105	93.8	456	Ŋ	AAE24530	Aae24530 Mouse PDE
11	1910	85.2		Ŋ	AAU79727	Aau79727 Human cyc
12	1903	84.8		4	AAU16967	Human
13	1787	79.7		ហ	ABB07912	Abb07912 Human PDE
14	1717	76.5	424	Ŋ	AAU79713	Aau79713 Human pho
15	1403.5	62.6		m	AAY93569	Amino
16	1403.5	62.6		4	AAU08675	Aau08675 Human pho
17	1403.5	62.6		4	AAG78915	
18	391.	62.0		m	AAY93567	Aay93567 Amino aci
13	83.	61.7	502	Ŋ	ABB09005	Abb09005 Human pho
20	1372.5	61.2		4	AAB36503	Human
21	1360.5	60.7	445	m	AAY93573	Amino
22	1358.5	9.09	44	ო	AAY93574	Amino
23	1358	60.5	451	m	AAY93575	5 Amino a
24	1338.5	59.7	4	m	AAY93572	572 Amino a
25	1270.5	56.6	413	m	AAY93571	Aay93571 Amino aci

Aau08676 Human pho Aau18681 Renal and Aau23004 Novel hum	Aau17039 Human nov Abu97296 Human pol nav93593 Amino aci	Amino Human	Aay27197 Rat PDE4A Abb98434 Amino aci		Aaw00090 Rat dunce					Ami		Abp96788 Human COP
AAU08676 AAU18681 AAU23004	AAU17039 ABU97296	AAY93568 AAB36504	AAY27197 ABP98434	AAR14836	AAW00090	AAY49803 AAB20614	AAR60605	AAY49825	AAB20636	AAY93994	AAE04745	ABP96788
444	400	u w 4	144	N	C) (n ro	N	N	m	ო	4	9
391 211 211	211	288 320	610	562	562	562 562	564	564	564	564	564	564
54.4 48.1 1.8	48.1	39.7	24.7	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5
1221 1079 1079	1079	891	7 C T 7 C T 7 C T	220	550	550 550	550	550	550	550	550	550
26 27 28	9 9 6	32 F) (L) (L)	3 6	37	8 6 8 6	40	41	42	43	44	45

ALIGNMENTS

Ā AAE24527 standard; protein; 426 entry) 04-OCT-2002 AAE24527; AAE24527

RESULT 1

(first

Human PDE7 protein.

Phosphodiesterase 7; PDE7; AIDS; acquired immune deficiency syndrome; immune system disease; enzyme; chronic obstructive pulmonary disease; T-cell related disease; autohimmune disorder; Crohn's disease; cancer; rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia; colitis; COPD; asthma; therapy; human.

Homo sapiens.

WO200226954-A2

04-APR-2002

28-SEP-2001; 2001WO-EP011303

28-SEP-2000; 2000EP-00402683

8

(WARN) WARNER LAMBERT

Soulard P;

WPI; 2002-479561/51. N-PSDB; AAD39376.

vel polypeptides exhibiting a higher phosphodiesterase PDE7 activity an endogenous full length PDE7, for screening of PDE7 inhibitors useful preventing and treating autoimmune disorders and inflammatory Novel

in prevent diseases.

Claim 2; Page 124-125; 137pp; English.

The invention relates to novel polypeptides exhibiting a higher phosphodiesterase 7 (PDB7) catalytic activity than endogenous full length beb57 and nucleic acid molecules encoding such polypeptides. Sequences of the invention are used for screening compounds that inhibit PDE7 activity, PDB7 inhibitors are used for manufacturing a pharmaceutical composition useful for the treatment or prevention of various pathological conditions such as diseases affecting the immune system, including acquired immune deficiency syndrome (AIDS), rejection of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
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                e.g. rheumatoid arthritis, inflammatory diseases such as respiratory inflammation diseases including chronic obstructive pulmonary disease (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's disease, colitis, pancreatitis and different types of cancers including leukaemia. The present sequence is human PDE7 protein
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ive 0; Mismatches 0;
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(WARN) WARNER LAMBERT

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                                                           Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity than endogenous full length PDE7, for screening of PDE7 inhibitors useful in preventing and treating autoimmune disorders and inflammatory diseases.
                                                                                                                                                                                                          The invention relates to novel polypeptides exhibiting a higher phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of the invention are used for screening compounds that inhibit PDE7
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                                                                                                                                                                                                                                                    the invention are used for screening compounds that inhibit PDE7 activity. PDE7 inhibitors are used for manufacturing a pharmaceutical composition useful for the treatment or prevention of various pathological conditions such as diseases affecting the immune system, including acquired immune deficiency syndrome (AIDS), rejection of transplant, autoimmune disorders such as T-cells related diseases for e.g. rheumatoid arthritis, inflammatory diseases such as respiratory inflammation diseases including chronic obstructive pulmonary disease (COPD), asthma, gastrointestinal inflammation diseases such as respiratory disease, colitis, pancreatitis and different types of cancers including leukaemia. The present sequence is human PDE7A2 protein
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100.0%; Pred. No. 6.8e-226;
tive 0; Mismatches 0;
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                                                                                                                                                                          Disclosure; Fig 1; 137pp; English.
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Phosphodiesterase 7; PDE7A1; AIDS; acquired immune deficiency syndrome; immune system disease; enzyme; chronic obstructive pulmonary disease; T-cell related disease; autoimmune disorder; Crohn's disease; cancer; rheunatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
                                                       colitis; COPD; asthma; therapy; human
                                                                                                                     28-SEP-2001; 2001WO-EP011303
                                                                                                                                     28-SEP-2000; 2000EP-00402683
                                                                                                                                                     (WARN ) WARNER LAMBERT CO.
        Human PDE7Al protein.
                                                                                                                                                                                    WPI; 2002-479561/51.
                                                                                       WO200226954-A2.
                                                                        Homo sapiens.
                                                                                                      04-APR-2002.
                                                                                                                                                                      Soulard P;
                                                                                                                                                                                                                               diseases
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The invention relates to novel polypeptides exhibiting a higher phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of the invention are used for screening compounds that inhibit PDE7 activity. PDE7 inhibitors are used for manufacturing a pharmaceutical composition useful for the treatment or prevention of various pathological conditions such as diseases affecting the immune system, including acquired immune deficiency syndrome (ADES), rejection of transplant, autoimmune disorders such as T-cells related diseases for transplant, autoimmune disorders such as T-cells related diseases for e.g. rheumation diseases including chronic obstructive pulmonary disease (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's disease, collitis, pancreatitis and different types of cancers including leukaemia. The present sequence is human PDE7Al protein Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity than endogenous full length PDE7, for screening of PDE7 inhibitors useful in preventing and treating autoimmune disorders and inflammatory Disclosure; Fig 1; 137pp; English.

Sequence 482 AA;

ö DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 116 LFSLHGLIEYFHLDMWKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240 GLESHLPLESROOMETQIGALILATDISRONEYLSLFRSHLDRGDLCLEDTRHRHLVLOM 300 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 356 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120 9 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES DOTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR Gaps . 0 Query Match 100.0%; Score 2243; DB 5; Length 482; Best Local Similarity 100.0%; Pred. No. 7.7e-226; Matches 426; Conservative 0; Mismatches 0; Indels 0 237 241 181 57 61 121 q à à g Dp ð 원 ò à

416 420 476 ALKCADICNPCRIWELSKOWSEKVTBEFFHOGDIEKKYHLGVSPLCDRHTESIANIQIGF 360 417 MIYLVEPLFTEWARFSNTRLSQIMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 357 ALKCADICNPCRIWELSKOWSEKVTEBFFHOGDIEKKYHLGVSPLCDRHTESIANIQIGF MIYLVEPLFTEWARFSNIRLSQIMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 426 482 QENRLS 477 QENRLS 361 421 301 g à 셤 Š 셤

AAW00094 standard; protein; 498 AA AAW00094

AAW00094;

(revised) 25-MAR-2003

(first entry) 09-OCT-1996

Human; glioblastoma cell; heat shock sensitivity; phosphodiesterase;
deficient yeast strain 10DAB; pTM22; rat DPD phosphodiesterase; pdel-;
bovine Ca2+/calmodulin dependent cAMP phosphodiesterase; heart; plasmid;
RAS2(vall9); pde2-; pTM3; pTM72; pRATDPD; pJC99; rolipram sensitive. CAMP phosphodiesterase encoded by plasmid pTM22 (ATCC 68601).

Homo sapiens.

18-JUN-1996

91US-00688352. 19-APR-1991; 90US-00511715. 20-APR-1990; (COLD-) COLD SPRING HARBOR LAB.

Colicelli JJ, Wigler MH;

WPI; 1996-299902/30. N-PSDB; AAT34376.

οĸ DNA mols. isolated from human glioblastoma cells - encode RAS-related cyclic nucleotide phosphodiesterase proteins.

Claim 4; Col 67-70; 101pp; English.

The sequences given in AAW00092-94 are encoded by plasmid fragments which contain human glioblastoma cell cDNA inserts which are capable of conteain human glioblastoma cell cDNA inserts which are capable of correcting the heat shock sensitivity of the phosphodiesterase deficient yeast strain 10DAB. Several cDNA's were isolated and sequenced. pTWA2 encodes a novel human gene. From computer analysis, pTW22 putatively encodes a protein homologous to various cAMP phosphodiesterases, such as the brownie Ca2+/calmodulin dependent cAMP phosphodiesterases, such as correct the heat chop phosphodiesterase. Sequences related to pTW22 were found to be expressed in human heart. Plasmid pTW22 was unable to correct the heat shock sensitivity of RAS2(vall) yeast strains. It thus appears that the cast shock sensitive to phenotypic reversion by mammalian cAMP phosphodiesterase clones than is the restrain. The inserts in the plasmids pTM3 and pTM72 were also characterised. These two different cAMP phosphodiesterase cDNA's insert and the pJC99 insert. Biochemical analysis of call lysates has celtablished that the cDNA's of pTM3 and pTM72, pJC44x and pRATDPD encode correct PF field.)

Sequence 498 AA;

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QENRLS
                                                                                                                                                                                       Sequence 498 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated RAS-related polypeptides and mammalian cyclic nucleotide phosphodiesterases, used for screening for agents which can modify complement or suppress genetic defects.
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Length 498;
                   Indels
100.0%; Score 2243; DB 2;
100.0%; Pred. No. 8.1e-226;
ive 0; Mismatches 0;
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94US-00206188.
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Best Local Similarity 100.
Matches 426; Conservative
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The present invention describes new isolated RAS-related polypeptides and mammalian cyclic nucleotide phosphodiesterases (PDBS) RAS-related polypeptides are capable of complementing a defective RAS function in yeast. The products can be used for screening for agents which can modify, complement or suppress a genetic defect in a biochemical pathway in which camp participates, or in a blochemical pathway which is controlled, directly or indirectly, by a RAS protein and other proteins affecting cell growth and maintenance. Developing agents that will selectively act upon PDBs is directed toward reproducing the desirable selectively act upon PDBs is directed toward reproducing the desirable contractility, anti-inflammation, yet without causing the undesirable effects of cyclic nucleotides, e.g. bronchodilation, increased myocardial contractility, anti-inflammation, yet without causing the undesirable effects, e.g. increased heart rate or enhanced lipolysis. The products can also be used for therapeutic, diagnostic and prognostic uses an also be wall and AAY49830, represent sequences used in the exemplification of the present invention
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100.0%; Pred. No. 8.1e-226;
iive 0; Mismatches 0;
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Col 85-88; 145pp; English.
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Matches 426; Conservative
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|||||| 493 QENRLS 498

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(COLD-) COLD SPRING HARBOR LAB.
Saccharomyces cerevisiae.
                                                 N-PSDB; AAA88175
                                         Colicelli JJ,
                   01-MAR-1994;
                         20-APR-1990;
                           19-APR-1991;
      JS6100025-A
            38-AUG-2000
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90US-00511715. 91US-0068B352. 94US-00206188

Wigler MH;

2000-531664/48.

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                                       is
                                                                                                                                                                                                              The present invention describes a purified and isolated DNA (I) which encodes a mammalian cyclic nucleotide phosphodiesterase and its an insert present in the plasmids ppDE46 (ATCC 69552), ppDE43 (ATCC 69551) or ppDE339 (ATCC 69550). The DNA molecules are used to modify, complement or suppress a genetic defect in a biochemical pathway in which CAMP participates and are also used as hybridisation probes. The present invention also describes methods for detecting mammalian genes encoding proteins which can function in microorganisms, particularly yeast, to modify, complement, or suppress a genetic defect associated with an
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Novel isolated DNA encoding a mammalian cyclic nucleotide phosphodiesterase is present in plasmids pPDE46, pPDE43 or pPDE339 and used to modify a genetic defect in a biochemical pathway in which CAMP
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100.0%; Pred. No. B.1e-226;
ive 0; Mismatches 0;
                                                                                                                                                                   Example 1; Col 85-88; 145pp; English
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The invention relates to novel polypeptides exhibiting a higher

thosphodiesterase 7 (PDE7) catalytic activity than endogenous full length

the invention are used for screening compounds that inhibit PDE7

the invention are used for screening compounds that inhibit PDE7

activity. PDE7 inhibitors are used for manufacturing a pharmaceutical

composition useful for the treatment or prevention of various

composition useful for the treatment or prevention of various

composition useful for the treatment or prevention of various

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composition useful for the inflammatory diseases including chronic obstructive pulmonary disease

composition diseases including chronic obstructive pulmonary disease

composition as thum, gastrointestinal inflammation diseases such as Crohn's

disease, colitis, pancreatitis and different types of cancers including

composition relative pulmonary diseases

composition as the present sequence is rat PDE7 protein
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                                                                                                                                                                                            Phosphodiesterase 7; PDE7; ALDS; acquired immune deficiency syndrome; immune system disease; enzyme; chronic obstructive pulmonary disease; T-cell related disease; autoimmune disorder; Crohn's disease; cancer; rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 1.38-212;
9; Mismatches 16; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 127-128; 137pp; English.
                                                                                                                                                                                                                                                                                   COPD; asthma; therapy; rat.
                                        AAE24529 standard; protein; 426 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 94.3%;
Best Local Similarity 94.1%;
Matches 401; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2001; 2001WO-EP011303.
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                                                                                                                                                              Rat PDE7 protein.
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e.g. rheumatoid arthritis, inflammatory diseases such as respiratory inflammation diseases including chronic obstructive pulmonary disease (COPD), athum, gastroointestinal inflammation diseases such as Crohn's disease, colitis, pancreatitis and different types of cancers includin leukaemia. The present sequence is rat PDE7a protein
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                                                                                                                                                          Length 428;
                                                                                                                                                                                                Indels
                                                                                                                                                      Score 2116; DB 5;
Pred. No. 1.3e-212;
9; Mismatches 16;
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COPD; asthma; therapy; mouse
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                                                                                                                                                                              Similarity
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                                                                                                                           Sequence 428
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Matches 401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity than endogenous full length PDE7, for screening of PDE7 inhibitors useful in preventing and treating autoimmune disorders and inflammatory
                                                                                     240
                                                                                                                                                                                      MIYLQEPLFTEWARFSDTRLSQTWLGHVGLNKASWKGLQRQQPSSEDASAAFELNSQLLT 420
                                                                                                                                                                                                                                          ALKCADICNPCRTWELSKOWSEKVTEEFFHOGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
                                                                                                                                                                                                                                                                MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLOREQSSSEDTDAAFELNSQLLP 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphodiesterase 7; PDE7a; AIDS; acquired immune deficiency syndrome;
                                     LFSIHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune system disease; enzyme; chronic obstructive pulmonary disease;
T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
                                                                                     VIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES
                                                                                                                       VIPWDIILSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES
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Soulard P;

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04-APR-2002

WO200226954-A2

28-SEP-2001; 2001WO-EP011303

(WARN) WARNER LAMBERT

28-SEP-2000; 2000EP-00402683

<u>ب</u> Soulard 2002-479561/51. N-PSDB; AAD39377 Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity than endogenous full length PDE7, for screening of PDE7 inhibitors useful in preventing and treating autoimmune disorders and inflammatory diseases.

Claim 2; Page 125-127; 137pp; English.

The invention relates to novel polypeptides exhibiting a higher phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length byDE7 and nucleic acid molecules encoding such polypeptides. Sequences of the invention are used for screening compounds that inhibit PDE7 activity. PDE7 inhibitors are used for manufacturing a pharmaceutical

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composition useful for the treatment or prevention of various pathological conditions such as diseases affecting the immune system, including acquired immune deficiency syndrome (AIDS), rejection of transplant, autoimmune disorders such as T-cells related diseases for e.g. Theumatoid arthritis, inflammatory diseases such as respiratory (Inflammation diseases including chronic obstructive pulmonary disease (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's disease, collitis, pancreatitis and different types of cancers including leukaemia. The present sequence is mouse PDB7 protein
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93.7%; Pred. No. 1.9e-211;
ive 13; Mismatches 14;
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Matches 399; Conservative
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RESULT 10

456 standard; protein; AAE24530 AAE24530

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AAE24530

(first entry) 04-0CT-2002

Mouse PDE7A2 protein.

Phosphodiesterase 7; PDE7A2; AIDS; acquired immune deficiency syndrome; immune system disease; enzyme; chronic obstructive pulmonary disease; real, related disease; autoimmune disorder; Crohn's disease; cancer; rheumatoid archritis; inflammatory disease; pancreatitis; leukaemia; colitis; COPD; asthma; therapy; mouse.

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WO200226954-A2

04-APR-2002

28-SEP-2001; 2001WO-EP011303

nucleotide phosphodiesterase, PDESA variant #3.

(first entry)

15-JUL-2002

AAU79727;

Human cyclic

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The invention relates to novel polypeptides exhibiting a higher phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of the invention are used for screening compounds that inhibit PDE7 activity, PDE7 inhibitors are used for manufacturing a pharmaceutical composition useful for the treatment or prevention of various pathological conditions such as diseases affecting the immune system, including acquired immune deficiency syndrome (ALDS), rejection of transplant, autoimmune disorders such as T-cells related diseases for e.g. rheumatoid arthritis, inflammatory diseases such as respiratory inflammatoin diseases including chronic obstructive pulmonary disease (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's disease, colitis, panceratitis and different types of cancers including leukaemia. The present sequence is mouse PDE7A2 protein
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                                                                                                                                                                                                                                                                              Disclosure, Fig 1; 137pp; English.
28-SEP-2000; 2000EP-00402683
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                                     (WARN ) WARNER LAMBERT
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Matches 399; Conserv
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The present invention relates to the isolation of novel cyclic nucleotide phosphodiesterase (PDE) proteins such as PDEBA, PDE7A3, TDPDE2A, TDPDE2B, TDPDE2B, TDPDE2B, TDPDE2B, TDPDESC, TOPDESC, TOPDESC, TOPDESC, TOPDESC, TOPDESC, TDPDESC, TDPDESC,
                                                                                                                                                            Human, cyclic nucleotide phosphodiesterase, PDE, T-cell activation; immune disorder; graft versus host disease; GVHD; T-cell lymphoma; acute lymphoblastic leukaemia; autorimmune disease; arthritis; insulin dependent diabetes mellitus; Crohn's disease; multiple sclerosis; scleroderma; mixed connective tissue disease; PDE8A; enzyme; variant.
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/note= "Encoded by CAT. This residue is illegible in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cyclic nucleotide phosphodiesterase polypeptides such as PDE8A, PDE7A3, TDPDE2A, TDPDE2B, TDPDE2C or TDPDE2E, that are involved in activation, useful for diagnosis and treatment of immune disorders.
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                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification"
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12-OCT-2000; 2000US-0240500P.
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SREBECK T.
SOBERLING S H.
RASCON A.
ZORAGHI R.
KUNZ S.
GONG K.
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Length 424;

Score 1910; DB 5; Pred. No. 5.3e-191;

85.2%; 99.5%;

Query Match Best Local Similarity

AAU79727 standard; protein; 424 AA.

RESULT 11 AAU79727 ID AAU79

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Sequence 424

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2000US-0236367P
2000US-0236368P
2000US-0236369P
2000US-0236370P
2000US-023602P
2000US-023703P
2000US-0237039P
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25-SEP-2000; 2
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27-SEP-2000; 2
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14-AUG-2000;
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20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide, fungicide; opthalmalogical; vulnerary; secreted protein; rhematoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                           180
                                         116
                                                                YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
                                                                                  117 YLRSSRFFRGTAVSNSLNILDDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 176
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                                                                                                                                                                    VIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 296
                                                                                                                                                                                                 GLFSHLPLESRQQMSTQ1GAL1LATD1SRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
                                                                                                                                                                                                            ALKCADICNPCRTWELSKOWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
                                                                                                                                                                                                                                                          ALKCADICHPCRIWELSKQWSEKVTEBFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGN 416
                      9
                                  LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS
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                    DOTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR
Gaps
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   AAU16967 standard; protein; 432 AA
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04-FEB-2000; 2000US-01864664P.
02-MAR-2000; 2000US-01864664P.
02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0199076P.
19-MAY-2000; 2000US-0199123P.
19-MAY-2000; 2000US-0209467P.
28-UNN-2000; 2000US-0214886P.
30-UNN-2000; 2000US-0214886P.
30-UUN-2000; 2000US-0216846P.
30-UUN-2000; 2000US-0216647P.
07-UUL-2000; 2000US-0216647P.
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 362; Conservative
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diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotexis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The

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Gaps 0; 180

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YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

61 65

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125 YLRSSRFFRGTAVSNSLNILDDDDYNGQAKCMLEKVGNWNRDIFLFDRLTNGNSLVSLTFH 184

LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 185 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES

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DOTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 124

1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR

Match 84,8%; Score 1903; DB 4; Length 432; Local Similarity 99.2%; Pred. No. 3e-190; les 361; Conservative 0; Mismatches 3; Indels

Query Match Best Loca Matches

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Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 208; 601pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000) 2000US-0249244P.
17-NOV-2000) 2000US-0249244P.
17-NOV-2000) 2000US-0249244P.
17-NOV-2000) 2000US-0249264P.
17-NOV-2000) 2000US-0249297P.
17-NOV-2000) 2000US-0249297P.
17-NOV-2000) 2000US-024929P.
17-NOV-2000) 2000US-024929P.
17-NOV-2000) 2000US-024929P.
17-NOV-2000) 2000US-02599P.
17-NOV-2000) 2000US-02599P.
17-NOV-2000) 2000US-025198P.
05-DEC-2000) 2000US-025186P.
06-DEC-2000) 2000US-025186P.
06-DEC-2000) 2000US-025186P.
06-DEC-2000) 2000US-025186P.
01-NOV-2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246573P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-024650P.
08-NOV-2000; 2000US-024661P.
                                                                                                                                                                                                                                                                                               2000US-0249212P
2000US-0249213P
2000US-0249214P
2000US-0249216P
2000US-0249216P
2000US-0249217P
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05-JAN-2001; 2001US-0259678P.
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                                                                                                                                                                                                                                                         17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
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N-PSDB; AAS26872
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17-NOV-2000; 2
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301 ALKCADICNPCRTWELSKOWSEKVTEEFFHOGDIEKKYHLGVSPLCDRHTESIANIQIGF

364

241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300

245 VIPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES

GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM

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Cyclic adenosine monophosphate; cAMP; cAMP phosphodiesterase type 7; PDE7a3; splice variant; transgenic; cardiant; antiinflammatory; antiallergic; antiasthmatic; antiinfertility; vaccine; enzyme.
                                                                                                                                                                                   Human PDE7a3 splice variant polypeptide.
                                         ABB07912 standard; protein; 336 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-2000; 2000EP-00109267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-2001; 2001WO-EP004785
                                                                                                                                     30-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MERE ) MERCK PATENT GMBH.
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                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2001.
                                                                                         ABB07912;
RESULT 13
                                                                 The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune
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WPI; 2002-034516/04.
                                                       Sequence 336 AA;
         N-PSDB; ABL58391
                   and asthma
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This represents a splice variant of cyclic adenosine monophosphate (cAMP) phosphodiesterase type 7 (PDE7a3). The polypeptide can be expressed by standard recombinant methodology. The PDE7a3 splice variant polypeptides and polynucleotides are useful for treating cardiovascular diseases, asthma, allergy, inflammatory diseases, fertility disorders and immunoregulator disorders. The polynucleotides are useful for producing transgenic animals, which include knock-in animals (in which an animal gene is replaced by human equivalent within the genome of the animal, useful in drug discovery process, for target validation. The PDE7a3 splice variant polypeptides and polynucleotides are useful as vaccines for inducing an immunological response in a mammal New polypeptide of splice variant of cyclic adenosine monophosphate phosphodiesterase type 7 and polynucleotides, useful as vaccines for inducing immune response against diseases e.g. cardiovascular diseases Claim 2; Page 33-36; 40pp; English.

ö TNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQ 180 NEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFH 330 NEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRIWELSKQWSEKVTEEFFH 240 QGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFTEWARFSNTRLSQTMLGHVGL 390 91 MIEKVGNWNPDIFIFDRITNGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYH 150 SQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIK 210 SQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIK 120 9 MLEKVGNWNFDIFLFDRLTNGNSLVSLTFFLFSLHGLIEYFHLDMMKLRRFLVMIQEDYH TNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLESROOMETOIGALILATDISRO Gaps ö Length 336; Indels NKASWKGLQREQSSSEDTDAAFELNSQLLPQENRLS 426 NKASWKGLOREOSSSEDTDAAFELNSOLLPOENRLS 336 . 0 79.7%; Score 1787; DB 5; 100.0%; Pred. No. 3e-178; tive 0; Mismatches 0; Matches 336; Conservative Local Similarity 211 61 121 181 331 241 391 301 Query Match 151 271 원 g ద g a à ò à à à

Human phosphodiesterase, PDE7A3 splice variant. AAU79713 standard; protein; 424 (first entry) 15-JUL-2002 AAU79713 RESULT

Human; cyclic nucleotide phosphodiesterase; PDE; T-cell activation; immune disorder; graft versus host disease; GVBD; T-cell lymphoma; acute lymphoblastic leuksemia; autoimmune disease; arthritis; insulin dependent diabetes mellitus; Crohm's disease; multiple sclerosis; scleroderma; mixed connective tissue disease; PDE7A3; enzyme; variant.

Homo sapiens

T cell .424
 /label= Unknown
 /note= "All residues represented by Xaa are illegible in the specification" s; New cyclic nucleotide phosphodiesterase polypeptides such as PDBSA, PDE7A3, TDPDE2A, TDPDE2B, TDPDE2C or TDPDE2E, that are involved in activation, useful for diagnosis and treatment of immune disorders. Kunz Zoraghi R, Rascon A, Soderling SH, cocation/Qualifiers 12-SEP-2000; 2000US-0232445P. 12-OCT-2000; 2000US-0240500P. 12-SEP-2001; 2001WO-US028503. BEAVO J A. SEEBECK T. SODERLING S H. Seebeck T, WPI; 2002-339862/37. RASCON A. ZORAGHI R. Glavas N; KUNZ S. GONG K. GLAVAS N. WO200222661-A2 Key misc_feature 21-MAR-2002 Ą (GLAV/) Gong K, (BEAV/) ZORA/) KUNZ/) SODE/) RASC/) GONG/ SEEB/) Beavo

Claim 2; Fig 8B; 165pp; English

The present invention relates to the isolation of novel cyclic nucleotide phosphodiesterase (PDE) proteins such as PDE8A, PDE7A3, TDPDE2A, TDPDE2B, TDPDE2B, TDPDE2B, TDPDE2C or TDPDE2E, TDPDE2B, TDPDE2B, TDPDE2C or TDPDE2E, TDPDE2B, TDPDE2B, TDPDE2C or TDPDE2B, TDPDE2B, TDPDE2B, TDPDE2C or TDPDE2B, TDPDE2B, TDPDE2B, TDPDE2B, TDPDE3B, orquence amount we encoused by Abkabbil. However, since the present assignment is of poor quality in the specification many of the residues are illegible

Sequence 424 AA;

ö 09 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR Gaps 0; Length 424; Indels 29; Score 1717; DB 5; Pred. No. 9.4e-171; 0; Mismatches 76.5%; 92.0%; Conservative Local Similarity ses 335; Conserv Query Match Matches

YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH

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121 LESLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

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ALKCADICNPCRXWELSKQXSEKVTEBFFHQGDIEXKYHLGVSPLCDRXTESIANIQIGN 416
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                                                                                          241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
                                                                                                            ALKCADICNPCRTWELSKOWSEKVTEEFFHOGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
177 LXSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHXAVHAADVTQAXHCYXKEPKLXNS 236
                             VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES
                                                           237 VXXXDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENXXWRSAVGLLRES
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Amino acid sequence of a human phosphodiesterase enzyme. AAY93569 standard; protein; 450 AA. (first entry) 25-SEP-2000 AAY93569

Phosphodiesterase; PDE-XIV; human; enzyme.

Homo sapiens EP1018559-A1 12-JUL-2000.

99EP-00308902 :09-NON-00

98GB-00028603 99GB-00022123 23-DEC-1998; 17-SEP-1999;

INC. (PFIZ) PFIZER (PFIZ) PFIZER

Fidock M;

WPI; 2000-433274/38. N-PSDB; AAA46651. Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.

Disclosure; Page 45-47; 104pp; English.

The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The phosphodiesterase polynucleotide and polypeptide may be used in the phosphodiesterase polynucleotide and polypeptide may be used in the inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and that role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV and and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV corposition for the treatment of a disoorder associated with inappropriate PDE-XIV expression and or activity and to screen for agents that can modulate PDE-XIV expression and to screen for agents that can may also be used as diagnostic agents for detecting the presence of PDE-XIV may also be used as diagnostic agents for detecting the presence of PDE-XIV may also be used as diagnostic agents for detecting the presence of PDE-XIV may also be used as diagnostic agents.

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                                                                                                                                                                                                                                                                                                                                                                                                             ALKCADICNPCRIWEMSKOWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGF 377
                                                                                                                                                                                                                                 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
                                                                                                                                                                                                                                                         138 LENTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASF 197
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XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA))
                                                                                                                                       1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR
                                                                                                                                                                            YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH
                                                                                                                                                                                                                                                                                     181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES
                                                                                                                                                                                                                                                                                                                                                                                               301 ALKCADICNPCRTWELSKOWSEKVTEEFFHOGDIEKKYHLGVSPLCDRHTESIANIQIGF
                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
                                                                     DB 3; Length 450;
                                                                                              Indels
                                                                   62.6%; Score 1403.5; DB 3; 62.6%; Pred. No. 7.9e-138; ive 66; Mismatches 87;
                                                                                                 Conservative
                                                                                    Local Similarity
                                             Sequence 450 AA;
                                                                                                 Matches 258;
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Query Match 100.0%; Score 2243; DB 1; Length 498; Best Local Similarity 100.0%; Pred. No. 5.4e-232; Matches 426; Conservative 0; Mismatches 0; Indels 0.
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1 DQTALYIRMLGDVRVRSRAG.....DTDAAFELNSQLLPQENRLS
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'GGDZ_6/ptodata/2/iaa/5B_COMB.pep:*

'GGDZ_6/ptodata/2/iaa/6A_COMB.pep:*

'GGDZ_6/ptodata/2/iaa/BECOMB.pep:*

'GGDZ_6/ptodata/2/iaa/PCTUS COMB.pep:*

'GGDZ_6/ptodata/2/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-47-379C-20
US-08-47-379C-20
US-09-36-1888-20
US-09-33-970-1
US-09-33-970-3
US-08-974-565C-9
US-09-255-748-9
US-09-255-748-9
US-08-942-521B-8
US-08-942-521B-8
US-08-44-379C-4
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US-08-206-188B-24
PCT-US91-02714-23
US-08-577-492-34
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Maximum Match 100%
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-079-630-34	US-08-942-521B-7	US-08-286-856C-2	US-08-472-831-2	US-08-286-856C-3	US-08-472-831-3	US-08-577-492-32	US-09-079-630-32	US-08-577-492-40	US-09-079-630-40	US-08-472-600-6	US-09-717-953-6	US-09-602-735B-2	US-08-472-600-5	US-09-717-953-5	US-08-577-492-35	US-08-474-379C-63	US-09-146-249A-63
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549	548.5	545	545	545	545	545	545	543	543	542	542	542	542	542	542	542	542
28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 20. Application US/07688352C
Patent No. 5527896
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Clouling by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/511,715
APPLICATION NUMBER: US 07/511,715
APPLICATION NUMBER: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 25447
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Illinois
COUNTRY: USA
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STRANDEDNESS: Six
US-07-688-352C-20
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                                                                                                                                                       121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
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                                                                           YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
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                                                                                                                                                                                LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS
                                                                                                                                                                                                                                     VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES
DOTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicell, John J.
TITLE OF INVENTION: CLOUNING BY COMPLEMENTATION AND RELATED TITLE OF INVENTION: PROCESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray (STRET: 233 South Wacker Drive/6300 Sears Tower CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: 05/08/474,379C FILLING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
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APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
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STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5977305
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ATTORNEY/AGENT INFORMATION:
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US-08-474-379C-20
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South Wacker Drive
                                                                                                                                                                                                                                                                                         Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                             100.0%; Score 2243; DB 2;
100.0%; Pred. No. 5.4e-232;
iive 0; Mismatches 0;
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APPLICATION NUMBER: US/09/146,249A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/09146249A
; Sequence 20, Application US/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchaell, O'Toole, Gere
STREET: 6300 Sears Tower, 233 Sout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 Sears Tower, 233 Sout
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
TELECOMMUNICATION INFORMATION:
TELEPRONE: (312) 474-6416
TELEFAX: (312) 474-0416
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                              LENGTH: 498 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                              Matches 426; Conservative
                                                                                                                                                                             , MOLECULE TYPE: protein US-08-474-379C-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QENRLS 426
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                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
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100.0%; Pred. No. 5.4e-232;
iive 0; Mismatches 0;
                                                                                                         Patentin Release #1.0, Version #1.25
                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEMCIN Release #1.0, Veric
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-MAR-1994
CLASSIPICATION DATA:
APPLICATION DATA:
TELESTATION DATA:
NAME: Clough, David W:
REGISTRATION NUMBER: 36107
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 1000 M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20:
                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 498 amino acids
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Matches 426; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLINGNSLVSLTFH 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSOSEIEVSVSARNIRRLLSFQR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 498;
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South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 2243; DB 3;
100.0%; Pred. No. 5.4e-232;
ive 0; Mismatches 0;
               PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTATION NUMBER: 36,107
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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Sequence 20, Application US/08206188B
Settle No. 6100025
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gers
STREET: 6300 Sears Tower, 233 Sout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                      TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 20: SEGUIENCE CHARACTERISTICS: LENGTH: 498 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 426; Conservative
                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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CLASSIFICATION:
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US-08-206-188B-20
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132 120 180

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80 GDIRLRGQTGVRAERRGSYPFIDFRLINSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139
                                                                                                                                                                       71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFFHLFSLHGLIEY 130
                                                                                                                                                                                                      131 FHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
                                                                                                                                                                                                                                                                                               SEO LAAAAAHDVDHPGVNQPPLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 318
                                                                       11 GDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRG
                                                                                                                                                                                                                                                                                                                                                                   191 IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLE
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Pred. No. 1.5e-50;
7; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: AL-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Coleman, Roger.
APPLICANT: Coleman, Roger.
APPLICANT: Fisher, Douglas A.
TITLE OF INVENTION: CYCLIC NUCLEOTIDE PHOSPHODIESTERASES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                           Indels
66.9%; Pred. No. 6.1e-85;
tive 34; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDEN COMPATIBLE
COMPUTER: DISKETTE
COMPUTER: DISKETTE
COMPUTER: DOS
SOFTWARE: FASTED FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Porter Dr.
CITY: Palo Alto
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/624,663
APPLICATION NUMBER: 08/624,663
FILING DATE: March 25,1996
ATTORNEY/AGENT INFORMATION:
NAME: MULTY, Lynn B.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PF-0057
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08974565C Patent No. 5932423 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.7%; Scor
32.6%; Pred
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  Best Local Similarity 66.9% Matches 160; Conservative
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Best Local Similarity 32.64
Matches 127; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: si
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CLONE: 1705952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 GDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRG
                                                                                                                                                                                                                                                                                                                                                                                               Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09330970
| Sequence 3, Application US/09330970
| Patent No. 6146876
| GENERAL INFORMATION:
| APPLICANT: Nobison, Keith E. |
| APPLICANT: Kapeller-Libermann, Rosana |
| APPLICANT: White, David |
| TITLE OF INVENTION: Phophodiseterase |
| TITLE OF INVENTION: 1999-06-11 |
| FARLIER APPLICATION NUMBER: US/09/330,970 |
| GURRENT FILING DATE: 1999-06-11 |
| FARLIER FILING DATE: 1999-06-11 |
| SARLIER FILING DATE: 1999-03-26 |
| NUMBER OF SEQ ID NOS: 40 |
| SOFTWARE: FASTSEQ for Windows Version 3.0 |
| SEQ ID NO 3 |
| LENGTH: 320 |
| TYPE: PRT |
| ORGANISM: Homo sapiens
                           6146876el Human Cyclic Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 EWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
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TITLE OF INVENTION: A No. 6146876el Human Cy.
TITLE OF INVENTION: A No. 6146876el Human Cy.
TITLE OF INVENTION: Phophodiesterase
FILE REFERENCE: 5800-28
CURRENT APPLICATION NUMBER: US/09/330,970
CURRENT FILING DATE: 1999-06-11
EARLIER FILING DATE: 1999-03-26
DATE: PRINCE FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 62.9
53; Conservative
                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-330-970-3
                                                                                                                                                                                                                                                                                                                                                                                                                                             253;
                                                                                                                                                                                                                                              SEQ ID NO 1
LENGIH: 502
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Matches
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8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR 63

DB 3; Length 320;

Score 871;

38.8%;

Query Match

Gaps

32;

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                                                                                                                                                                                 64 SSR-----FFRGTAVSNSLNI-----LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG
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                                                                                                        32;
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                                                               Length 610;
                                                                                                          Indels
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APPLICANT: Wigler, Michael H.
APPLICANT: Collicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Rel;
TITLE OF INVENTION: Processes
INDMER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Marshall, STREET: TWO First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBRIE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
FILING DATE: 19910419
                                                           Query Match

24.7%; Score 555; DB 3;
Best Local Similarity 32.6%; Pred. No. 1.5e-50;
Matches 127; Conservative 77; Mismatches 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 PMCDKHTASVEKSOVGFIDYIVHPLWETWA 410
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REGISTRATION NUMBER: 25447
REFERENCE/COCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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CLASSIFICATION:
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US-09-255-748-9
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Sequence 9, Application US/09255748
Patent No. 6080548
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Coleman, Roger
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Fisher, Douglas A.
TITLE CA INVENTION:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: F815EQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/255,748
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REFERENCE/DOCKET NUMBER: PF-0057-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,565
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-09-255-748-9
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COUNTRY: United States of America ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,
FILING DATE: 10 March 1993
CLASSIFICATION: 536
                                                                                                                                                                                                                                                    : 562 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 122; Conservative
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Best Local Similarity
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CITY: Chicago
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US-08-474-379C-4
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                                                                                                                                                                                               Length 562;
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Patent No. 5932477
GENERAL INFORMATION:
APPLICANT: Livi, George P.
APPLICANT: McLaughlin, Megan M.
APPLICANT: Torphy, Theodore J.
TITLE OF INVENTION: Human Brain Phosphodiesterase
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,521B
FILING DATE: October 2, 1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SmithKline Beecham Corporation STREET: Corporate Patents/ P.O.Box 1539 STREET: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 TASVEKSOVGFIDYIVHPLWETWA 457
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/446,386
FILING DATE: 22 May 1995
CLASSIFICATION: 536
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                           LENGTH: 562 amino acids TYPE: AMINO ACID
                                                                                                                               MOLECULE TYPE: protein US-07-688-352C-4
                                                                                                                     linear
                                                                                                                   TOPOLOGY:
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374 NYTDRIQVLRNMYHCADLSNPTKSLELYRQWTDRIMBEFFQQGDKERERGMEISFMCDKH 433
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Patent No. 5977305
GENERAL INPORMATION:
APPLICANT: Wighler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED TITLE OF INVENTION: PROCESSES
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.5%; Score 550; DB 2; Length 562; 31.8%; Pred. No. 4.5e-50; tive 84; Mismatches 152; Indels
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STREET: 233 South Wacker Drive/6300 Sears Tower
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ATTORNEY AGENT INFORMATION:
NAME: Elizabeth J. Hecht
REGISTRATION UNBER: 41,824
REFERRICG DOCKET NUMBER: 950145C1FWC
TELECOMMUNICATION INFORMATION:
TELERAX: (215) 270-5009
TELERAX: (215) 270-5009
TELERAX: (215) 270-5009
SEQUENCE CHARACTERISTICS:
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59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
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4.5e-50;
               3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
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                                                                                                                                                            RY: United States of America 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 31.8
Matches 122; Conservative
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                              STREET: 0. Thicago
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       ADDRESSEE:
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US-08-206-188B-4
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Patent No. 6062240

GENERAL INFORMATION:
APPLICANT: Wigher, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE: 85

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.5%; Score 550; DB 2; Length 562;
31.8%; Pred. No. 4.5e-50;
tive 84; Mismatches 152; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/171,715
PRIOR APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991
ATTOMENTY/AGRAY INFORMATION:
ATTOMENTY/AGRAY INFORMATION:
ANAMERICATION PATA:
ATTOMENTY/AGRAY INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CIOUGH, DAVIG W.
REGISTRATION NUMBER: 36,107
REFERENCE DOCKET NUMBER: 27866/32771
TELECOMUTUCATION INFORMATION:
TELEPENS: (312) 474-6300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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US-09-146-249A-4
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MEDIUM TYPE:
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Best Local Simil
Matches 122; (
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 Cloning by Complementation and Related
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                                                                                                                      CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-MAR-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-AFR-1990
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36107
TELEFRAX: 312-474-6300
TELEFRAX: 312-474-0448
                                                                        3: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
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                   Processes
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INFORMATION FOR SEQ ID NO: 4:
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amino acid
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LENGTH: 562 amino ació
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                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
STREET: 6300 Sears To
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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Matches 122; Conserva
                                                                                                              Chicago
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GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 562;
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                                                                                                                   NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: PCT/US91/0271/FILING DATE: 19910419
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CLASSIFICATION: 435
RICK APPLICATION DATE:
APPLICATION NUMBER: US 07/511,715
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Sequence 4, Application PC/TUS9102714

RESULT 14 PCT-US91-02714-4

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256 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406-0939

ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCH IN PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PARCHILL Release #1.0, Version #1.25
SOFTWARE: PAPELICATION DATA:
FILING DATE: OCCODER 2, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Livi, George P.
APPLICANT: McLaughlin, Megan M.
APPLICANT: Torphy, Theodore J.
APPLICANT: Torphy, Theodore J.
APPLICANT: Human Brain Phosphodiesterase NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS.
ADDRESSES: SmithKline Beecham Corporation STRET: Corporate Patents/ P.O.Box 1539 CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 41,824
REFERENCE/DOCKET NUMBER: P50145C1FWC
434 TASVEKSQVGFIDYIVHPLWETWA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/446,386
FILING DATE: 22 May 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
RELING DATE: 10 March 1993
CLASSIFICATION 536
ATTOMNEY AGENT INFORMATION:
ATTOMNEY BLIZABECH J. Hecht
REGISTRATION NUMBER: 41,824
                                                                                                                            ; Sequence 2, Application US/08942521B
; Patent No. 5932477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5009
TELEFAX: (215) 270-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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Best Local Similarity
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376 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFRQQGDKERERGMEISPMCDKH 290 DTRHRHLVLQMALKCADICNPCRIWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 350 TESIANIQIGEMTYLVEPLETEWA 373 à d ŏ qq

Search completed: May 26, 2004, 09:29:02 Job time : 24 secs

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SEIEASVSAR
SEIEVSVSAR
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MLEKVGNWNF
MLEKVGNWNF
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